



UNITED STATES ENVIRONMENTAL PROTECTION
AGENCY

OFFICE OF CHEMICAL SAFETY
AND POLLUTION PREVENTION

MEMORANDUM

SUBJECT: Human Health and Environmental Risk Assessment for the New Product OX5034 Containing the Tetracycline-Repressible Transactivator Protein Variant (tTAV-OX5034; New Active Ingredient) Protein, a DsRed2 Protein Variant (DsRed2-OX5034; New Inert Ingredient), and the Genetic Material (Vector pOX5034) Necessary for Their Production in OX5034 *Aedes aegypti*; Data and Information Were Provided in Support of a FIFRA Section 5 Application.

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I. OVERVIEW

Oxitec Ltd., (Oxitec or the applicant) requests an Experimental Use Permit (EUP) under FIFRA section 5 for a new end-use product OX5034 containing a variant of the new active ingredient tetracycline-repressible transactivator (tTAV-OX5034) protein, a variant of the new inert ingredient DsRed2 protein (DsRed2-OX5034), and the genetic material (vector pOX5034) necessary for their production in OX5034 *Aedes aegypti* (Yellow Fever mosquito). Oxitec requests this EUP to evaluate whether the product is efficacious in suppressing naturally occurring *Ae. aegypti* populations under field conditions.

OX5034 is described as a species-specific female-lethal trait that results in emergence of all-male progeny in the absence of tetracycline in the larval diet. The pesticidal effect of OX5034 is species-specific as it only affects the reproductive success of *Ae. aegypti* through mating between OX5034 *Ae. aegypti* males and *Ae. aegypti* females that are already present in the release area. OX5034 homozygous males will be released into the environment where they mate with females that are already present in that area. Only female offspring are killed while OX5034 hemizygous males survive to pass on the OX5034 female-lethal trait further. Unlike female mosquitoes, male mosquitoes do not bite humans. With continued field releases of OX5034 homozygous males, the *Ae. aegypti* population in the treatment area is thought to progressively decline due to the reduced number of females emerging at each consecutive generation. In addition, OX5034 also expresses DsRed2-OX5034, a variant of the DsRed fluorescent protein form *Discosoma* spp., that allows for the visual identification of OX5034 hemizygous larvae collected from the field.

With this application, Oxitec requests a 24-month permit for a cumulative annual test area of 5,000 acres. The area is divided into multiple test and control plots within Monroe, Co., Florida and Harris, Co., Texas. Under the EUP, Oxitec is planning to test the efficacy of the product by deploying eggs and adult males homozygous for the OX5034 traits. This memorandum contains BPPD's risk assessments of the end-use product OX5034.

II. SCIENCE ASSESSMENT

A. Product Characterization

The manufacturing process and the characteristics of the resulting pesticide product provide the foundation for assessing its risk for human health and the environment. This section describes the OX5034 *Ae. aegypti* strain, how the strain was developed, the purpose of the genetic elements integrated into the mosquito genome, and the mechanisms underlying the female-specific lethality.

1. Transformation system and genetic elements

The OX5034 *Ae. aegypti* line was developed in 2013 by transformation of a "Latin American *Ae. aegypti* wild-type" strain (LWT) with the vector pOX5034. The strain was subsequently backcrossed several times to obtain the OX5034 homozygous *Ae. aegypti* for which the EUP is sought. The background of the LWT strain is comprised of genetics from ten separate *Ae. aegypti* colonies. These colonies were established from mosquitoes that were collected in the Mexican State of Chiapas in 2006 [ADDIN

EN.CITE <EndNote><Cite><Author>Wise de

Valdez</Author><Year>2011</Year><RecNum>196</RecNum><DisplayText>(Wise de Valdez et al.

2011)</DisplayText><record><rec-number>196</rec-number><foreign-keys><key app="EN" db-

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keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Wise de Valdez,

M. R.</author><author>Nimmo, D.</author><author>Betz, J.</author><author>Gong, H.

F. James, A. A. Alphey, L. Black, W. C. th Department of Microbiology, Immunology, and Pathology, Colorado State University, Fort Collins, CO 80523-1682, USA. Genetic elimination of dengue vector mosquitoes Proc Natl Acad Sci U S A Proc Natl Acad Sci U S A 4772-5 108 12 2011/03/09 Aedes/*genetics/virology Animals Animals, Genetically Modified/*genetics/virology Dengue/epidemiology/*transmission Female Insect Vectors/*genetics/virology Male Pest Control, Biological/*methods 2011 Mar 22 1091-6490 (Electronic)0027-8424 (Linking) 21383140 https://www.ncbi.nlm.nih.gov/pubmed/21383140 PMC3064365 10.1073/pnas.1019295108

The OX5034 expression cassette contains several genetic elements in addition to the sequences coding for the active ingredient tetracycline-repressible transactivator protein (tTAV-OX5034) and the inert ingredient DsRed2-OX5034. Briefly, minimal expression of *tTAV-OX5034* is driven by the DmHsp70 minimal promoter and 5' UTR from *D. melanogaster* located downstream of a tetracycline-responsive operator (*tetO₇*). This basal expression of the protein is required for the initiation of the positive feedback loop that is characteristic of the Tet-OFF system (Unit II.A.2.). Dimeric tTAV (cleaved variant of tTAV-OX5034) binds to the *tetO₇* operator and enhances expression of *tTAV-OX5034* in the absence of tetracyclines. tTAV-OX5034 is a chimeric fusion protein that consists of three basic functional units: At the N-terminus, a modified version of the *Ae. aegypti doublesex* gene (*Aeadsx*) [ADDIN EN.CITE ADDIN EN.CITE.DATA], followed by ubiquitin (*D. melanogaster*), and tTAV, which itself is a fusion of the tetracycline-binding domain protein (tetR) and the viral tegument protein 16 (VP16; transcriptional activator) from the Herpes simplex virus-1 (HSV-1) [ADDIN EN.CITE ADDIN EN.CITE.DATA].

DsRed2-OX5034 is virtually identical to DsRed2 [ADDIN EN.CITE ADDIN EN.CITE DATA] (Yanushevich et al. 2002) 36 (Yanushevich et al. 2002) 36 Yanushevich, Y. G. Staroverov, D. B. Savitsky, A. P. Fradkov, A. F. Gurskaya, N. G. Bulina, M. E. Lukyanov, K. A. Lukyanov, S. A. Shemyakin and Ovchinnikov Institute of Bioorganic Chemistry RAS, Moscow, Russia. A strategy for the generation of non-aggregating mutants of Anthozoa fluorescent proteins FEBS Lett 11-4 511 1-3 2002/02/01 Amino Acid Substitution/genetics Animals Cloning, Molecular/*Cnidaria/chemistry/genetics Color

<keyword>Electrophoresis, Polyacrylamide
Gel</keyword><keyword>Fluorescence</keyword><keyword>Luminescent
Proteins/chemistry/*genetics/*metabolism</keyword><keyword>Molecular
Weight</keyword><keyword>Mutagenesis, Site-
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urls><url>https://www.ncbi.nlm.nih.gov/pubmed/11821040</url></related-urls></urls><electronic-
resource-num>10.1016/s0014-5793(01)03263-x</electronic-resource-
num></record></Cite></EndNote>], but in addition contains a bipartite nuclear localization sequence
(NLS) and linker sequences at its N- and C-terminus. The expression of the *DsRed2-OX5034* gene is
driven by the IE1 promoter and Hr5 enhancer, both of which are derived from *A. californica*
nucleopolyhedrovirus (AcNPV). *DsRed2-OX5034* is the fluorescent marker that allows for visual
identification of *Ae. aegypti* individuals carrying the OX5034 genetic cassette in larvae collected from the
field. Expression from these regulatory elements is expected to be constitutive, although tTA
overexpression in insects has also been observed to positively affect the expression of fluorescence
markers located on the same genetic construct. For example, in the transgenic *Ae. aegypti* strain LA513,
which expresses different variants of the *tTAV-OX5034* and *DsRed2-OX5034* genes, tTAV presence is
reported to positively affect *DsRed2* expression from a *D. melanogaster* Actin 5C promoter [ADDIN
EN.CITE
<EndNote><Cite><Author>Alphey</Author><Year>2015</Year><RecNum>198</RecNum><DisplayT
ext>(Alphey 2015)</DisplayText><record><rec-number>198</rec-number><foreign-keys><key
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type><contributors><authors><author>Alphey,
Luke</author></authors></contributors><titles><title>Expression system for insect pest
control</title></titles><dates><year>2015</year></dates><publisher>Google
Patents</publisher><urls></urls></record></Cite></EndNote>]. Similarly, positive correlation between
tTA expression and expression of the fluorescent marker ZsGreen was observed in a transgenic strain of
D. melanogaster [ADDIN EN.CITE
<EndNote><Cite><Author>Knudsen</Author><Year>2020</Year><RecNum>137</RecNum><Display
Text>(Knudsen et al. 2020)</DisplayText><record><rec-number>137</rec-number><foreign-keys><key
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type><contributors><authors><author>Knudsen, K. E.</author><author>Reid, W.
R.</author><author>Barbour, T. M.</author><author>Bowes, L. M.</author><author>Duncan,
J.</author><author>Philpott, E.</author><author>Potter, S.</author><author>Scott, M.
J.</author></authors></contributors><auth-address>North Carolina State University.North
Carolina State University mjscott3@ncsu.edu.</auth-address><titles><title>Genetic Variation and
Potential for Resistance Development to the tTA Overexpression Lethal System in
Insects</title><secondary-title>G3 (Bethesda)</secondary-title></titles><periodical><full-title>G3
(Bethesda)</full-
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technique</keyword><keyword>tetracycline

transactivator</keyword></keywords><dates><year>2020</year><pub-dates><date>Feb 5</date></pub-dates></dates><isbn>2160-1836 (Electronic)2160-1836 (Linking)</isbn><accession-num>32019873</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/32019873</url></related-urls></urls><electronic-resource-num>10.1534/g3.120.400990</electronic-resource-num></record></Cite></EndNote>].

Characterization of the genomic DNA isolated from OX5034 homozygous *Ae. aegypti*, using restriction enzyme digestion and Southern blot analysis, indicate that the genetic cassette from plasmid pOX5034 inserted as a single, intact copy into the mosquito genome (MRID 50889401). The genomic locus of insertion was identified by sequencing the genomic region flanking the insertion site at the 5' end and comparison of that sequence with the *Ae. aegypti* AagL3 genome assembly (2014) deposited in VectorBase (www.vectorbase.org). Based on the data provided, it is unlikely that the inserted OX5034 gene cassette disrupts any open reading frames within the genome of OX5034 *Ae. aegypti*. To obtain a homozygous strain, the originally transformed strain was backcrossed several times. In doing so, any piggyBac™ vector backbone that may have inserted into the genome, in addition to the expression cassette, would be segregated out. PCR analysis of the OX5034 genome using backbone-specific primers demonstrated the absence of backbone DNA in the OX5034 genome. The observation that the DsRed2-OX5034 fluorescence phenotype segregates in a Mendelian pattern of inheritance indicates the stability and inheritance of the inserted DNA across several generations.

Information on the genetic stability of the OX5034 traits was provided, which supports the conclusion that integration of the genetic cassette is stable. The OX5034 expression cassette was inserted into the *Ae. aegypti* genome using the piggyBac™ transposon system (MRID 50889424). The specific system used in the creation of OX5034 is comprised of two components that were co-transformed into *Ae. aegypti* embryos via microinjection: a vector carrying the genetic cassette (pOX5034) and mRNA encoding for the piggyBac™ transposase enzyme that facilitates excision of the cassette from the vector and integration into the mosquito genome. Briefly, the genetic cassette that codes for *tTAV-OX5034* and *DsRed2-OX5034* and its regulatory elements was cloned between two inverted terminal repeat sequences (ITRs), which were originally derived from the transposon of the cabbage looper moth *Trichoplusia ni* [ADDIN EN.CITE ADDIN EN.CITE.DATA]. The piggyBac™ transposase recognizes the ITRs and integrates the intervening DNA into the genome, preferentially at TTAA sites, although non-canonical integration has also been observed [ADDIN EN.CITE ADDIN EN.CITE.DATA]. The piggyBac™ transposon system has generally been found to result in the integration of intact genetic cassettes. Re-excision from the genome is not expected to occur as the piggyBac™ transposase is only transiently expressed in transformed cells and because the integrated cassette does not itself encode for a transposase enzyme. Other transgenic *Ae. aegypti* that were created using the piggyBac™ transposon system have been reported to be genetically stable, which has been hypothesized to be due to a low proportion of transposon-specific piRNAs in this mosquito species [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Relatedly, remobilization of the OX5034 expression cassette in OX5034 *Ae. aegypti* has not been observed in over 27 generation equivalents.

2. Pesticidal activity of the active ingredient tTAV-OX5034

OX5034 female lethality is attributed to the overexpression of the tTAV-OX5034 protein, a process that is thought to interfere with the transcriptional machinery of the insect and consequently normal cellular function. This tTAV-associated effect is commonly referred to as transcriptional squelching [ADDIN EN.CITE

<EndNote><Cite><Author>Gill</Author><Year>1988</Year><RecNum>260</RecNum><DisplayText

>(Gill and Ptashne 1988)</DisplayText><record><rec-number>260</rec-number><foreign-keys><key app="EN" db-id="2t2pdevxize0spe5fsvxsfflfd5zwa2ex2s5" timestamp="1586876929">260</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Gill, G.</author><author>Ptashne, M.</author></authors></contributors><auth-address>Department of Biochemistry and Molecular Biology, Harvard University, Cambridge, Massachusetts 02138.</auth-address><titles><title>Negative effect of the transcriptional activator GAL4</title><secondary-title>Nature</secondary-title></titles><periodical><full-title>Nature</full-title><abbr-1>Nature</abbr-1></periodical><pages>721-4</pages><volume>334</volume><number>6184</number><edition>1988/08/25</edition><keywords><keyword>Binding Sites</keyword><keyword>DNA, Fungal/metabolism</keyword><keyword>DNA, Recombinant</keyword><keyword>DNA-Binding Proteins</keyword><keyword>Fungal Proteins/*pharmacology</keyword><keyword>Gene Expression Regulation/drug effects</keyword><keyword>Genes, Fungal</keyword><keyword>Plasmids</keyword><keyword>Promoter Regions, Genetic</keyword><keyword>*Saccharomyces cerevisiae Proteins</keyword><keyword>*Transcription Factors</keyword><keyword>Transcription, Genetic/*drug effects</keyword></keywords><dates><year>1988</year><pub-dates><date>Aug 25</date></pub-dates></dates><isbn>0028-0836 (Print)0028-0836 (Linking)</isbn><accession-num>3412449</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/3412449</url></related-urls></urls><electronic-resource-num>10.1038/334721a0</electronic-resource-num></record></Cite></EndNote>]. Others have suggested that the overexpression of tTAV leads to the stochastic differential expression of genes in the transgenic organism in a manner that is specific to the site of transgene integration [ADDIN EN.CITE ADDIN EN.CITE.DATA]. The latter may therefore also contribute to the lethal effect.

Overexpression of *tTAV-OX5034* is achieved through a gene circuit that is based on the “Tet-OFF” system that was first described in *E. coli* [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Here, basal *tTAV-OX5034* expression is enhanced through a positive feedback loop that can be suppressed through the addition of tetracycline or its analogs to the larval diet. Briefly, basal expression of *tTAV-OX5034* is driven by the DmHsp70 minimal promoter, which is required to initiate the positive feedback loop. Once translated, tTAV-OX5034 is cleaved to release tTAV, which dimerizes and, in the absence of tetracyclines, binds to *tetO₇*, enhancing the expression of *tTAV-OX5034* [ADDIN EN.CITE <EndNote><Cite><Author>Fu</Author><Year>2007</Year><RecNum>81</RecNum><DisplayText>(Fu et al. 2007)</DisplayText><record><rec-number>81</rec-number><foreign-keys><key app="EN" db-id="2t2pdevxize0spe5fsvxsfflfd5zwa2ex2s5" timestamp="1586391004">81</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Fu, G. L.</author><author>Condon, K. C.</author><author>Epton, M. J.</author><author>Gong, P.</author><author>Jin, L.</author><author>Condon, G. C.</author><author>Morrison, N. I.</author><author>Dafa'alla, T. H.</author><author>Alphey, L.</author></authors></contributors><auth-address>Oxitec Ltd, Oxford OX14 4RX, EnglandUniv Oxford, Dept Zool, Oxford OX1 3PS, England</auth-address><titles><title>Female-specific insect lethality engineered using alternative splicing</title><secondary-title>Nature Biotechnology</secondary-title><alt-title>Nat Biotechnol</alt-title></titles><alt-periodical><full-title>Nat Biotechnol</full-title></alt-periodical><pages>353-357</pages><volume>25</volume><number>3</number><keywords><keyword>genetic system</keyword><keyword>autocidal control</keyword><keyword>transformer

gene</keyword><keyword>in-vivo</keyword><keyword>fly</keyword><keyword>eradication</keyword><keyword>conservation</keyword><keyword>expression</keyword><keyword>management</keyword><keyword>dominant</keyword></keywords><dates><year>2007</year><pub-dates><date>Mar</date></pub-dates></dates><isbn>1087-0156</isbn><accession-num>WOS:000244748300028</accession-num><urls><related-urls><url><Go to ISI>://WOS:000244748300028</url></related-urls></urls><electronic-resource-num>10.1038/nbt1283</electronic-resource-num><language>English</language></record></Cite></EndNote>] (Figure 1). Because the tTAV homodimer preferentially binds to tetracycline over *tetO*₇, the addition of tetracycline to the system can quench *tTAV-OX5034* expression. Thus, in order to be able to sustain a OX5034 homozygous *Ae. aegypti* colony in the laboratory, tetracycline must be added to the rearing medium, as no intervention would lead to the death of OX5034 females.

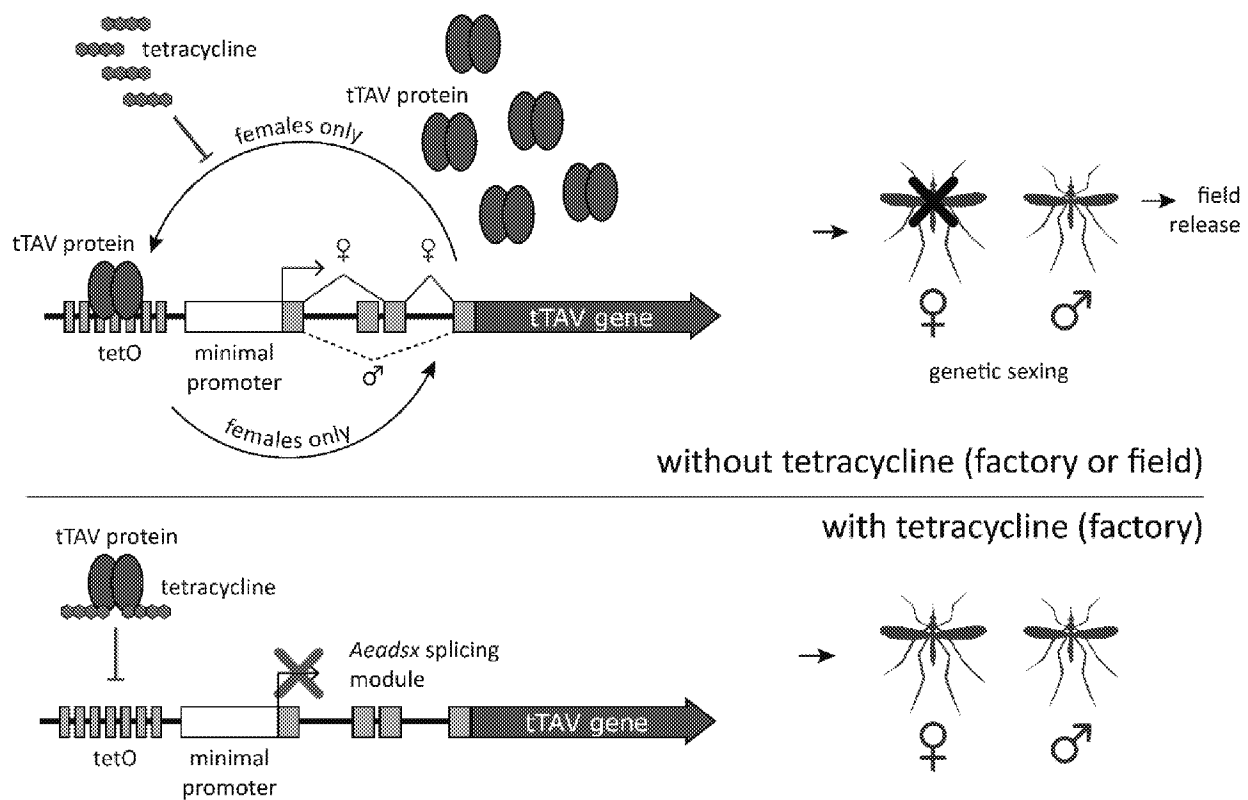


Figure 1. Schematic representation of the OX5034 female-lethal trait mediated through sex-specific *tTAV-OX5034* expression. **Top:** In the absence of tetracyclines, basal expression of *tTAV-OX5034* in female OX5034 *Ae. aegypti* results in the production of the tTAV-OX5034 protein. The *Aeadsx* splicing module located at the 5'-end of the *tTAV-OX5034* gene is alternately spliced in males and females, leading to the preferential expression of the full-length *tTAV-OX5034* mRNA isoform in females. Once the protein is translated it is cleaved by endogenous deubiquitinases at the UBQ-tTAV junction, releasing tTAV. tTAV then dimerizes (purple ovals). The positive feedback loop is closed when the VP16-domains of the tTAV protein bind to the *tetO*₇ operator, which enhances the expression of the *tTAV-OX5034* gene. Through this mechanism of overexpression, cellular functions are affected resulting in cell death in the developing larvae. **Bottom:** In the absence of tetracyclines, basal expression of *tTAV-OX5034* still occurs. Because tTAV preferentially binds to tetracycline than to *tetO*₇, expression is not enhanced.

3. Conditional female-specific expression of *tTAV-OX5034*

The genetic construct that was integrated into the *Ae. aegypti* genome was designed such that the active ingredient is primarily expressed in female mosquitoes. Briefly, female-specific lethality of *tTAV-OX5034* is achieved by inclusion of a splicing module upstream of the genetic sequence coding for *tTAV*. The splicing module is derived from the *Ae. aegypti Aeadsx (doublesex)* gene, which is differentially spliced in males and females as part of the sexual differentiation pathway [ADDIN EN.CITE ADDIN EN.CITE.DATA]. The genetic sequence of exon 5b of *Aeadsx* in OX5034 was minimally altered from exon 5b present in the native gene. OX5034 females produce two mRNA isoforms of *tTAV-OX5034*, F1 and F2, and males primarily produce a single M isoform (Figure 2). Both the F1 and M isoforms contain a premature stop codon and are unlikely to be translated. The F2 isoform produced in OX5034 females is being translated into *tTAV-OX5034* and thus, the pesticidal mode of action is female-specific.

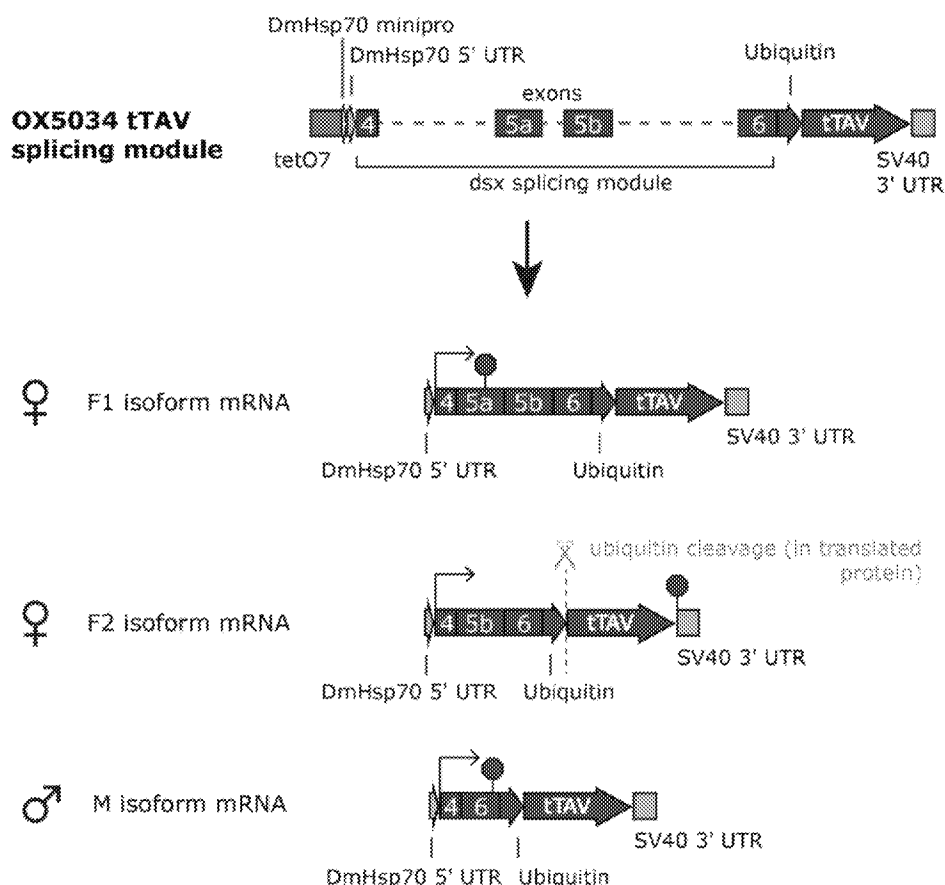


Figure 2. Schematic representation of the splicing module in *tTAV-OX5034*. The *Aeadsx* splice module consists of exons 4, 5a, 5b, and 6, together with the fragments of *Aeadsx* introns 4, 5, and 6. The arrow indicates the position of the start codon and the red octagon indicates that of a stop codon.

Oxitec provided data that demonstrate that the minimally altered *Aeadsx* splice module in *tTAV-OX5034* results in the differential expression of the mRNA in males and females and that the F2 isoform that codes for the active ingredient is primarily expressed in female mosquitoes. A study was presented that evaluated female-specific splicing of the *tTAV-OX5034* mRNA in OX5034 *Ae. aegypti*. Using *tTAV-OX5034*-specific primers, female OX5034 pupae were shown to express both female mRNA isoforms, F1 and F2, with F2 being the most abundant. OX5034 females do not produce the male isoform M, or this

isoform was present below the limit of detection. Comparable results were obtained in the LWT background when analyzing the isoforms of the native *Aeadsx* transcript.

Male OX5034 pupae were shown to express the M isoform as well as a small amount of the F2 isoform. The study remarks that this may be the result of ineffective splicing that occurs at low levels (Unit II.A.4.; MRID 50889419). While mRNA abundance in adult males was not evaluated, the F2 isoform is likely also transcribed in adult males as the tTAV-OX5034 protein is detected in adult males at 1- and 6 days post eclosion (Unit II.A.4.b.). If the F2 isoform of the native *Aeadsx* gene is expressed in male LWT pupae, abundance is below the detection limit of this assay.

4. Protein abundance

The abundance of the tTAV-OX5034 and DsRed2-OX5034 proteins was determined in OX5034 male mosquitoes at several life stages. The protein content in homozygous adult males is the most relevant for determining the amount of pesticide applied during the experimental program as these individuals will be released into the environment; while eggs will also be deployed, they are contained in the mosquito rearing boxes from which adult homozygous males will emerge.

As presented in Unit II.A.3., OX5034 male pupae, like OX5034 females, produce the F2 mRNA isoform of *tTAV-OX5034* and thus it is conceivable that adult males also produce the tTAV-OX5034 protein. Once translated, tTAV-OX5034 is thought to be cleaved at the UBQ-tTAV junction to release the tTAV protein which, once dimerized, will initiate the positive feedback loop characteristic of the Tet-OFF gene circuit (Figure 1) [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Consequently, three variations of the tTAV-OX5034 protein may be present within the mosquito: tTAV-OX5034 (full-length protein), monomeric tTAV (cleaved), and dimerized tTAV (the transcriptionally active form of the protein). In addition to tTAV-OX5034, homozygous males were expected to produce DsRed2-OX5034 protein, as the marker can be visually identified in hemizygous *Ae. aegypti* male larvae and because *DsRed2-OX5034* is under the control of a constitutive promoter (Units II.A.1 and II.A.6.).

a. DsRed2-OX5034

DsRed2-OX5034 protein abundance was determined in the lysate of homo- and hemizygous OX5034 males at the larval, pupal, and two adult life stages. Mosquitoes were reared in the absence of tetracyclines. Protein abundance was quantified using immunoblot analysis with polyclonal primary antibody for DsRed2 (TaKaRa; Clontech) in mosquito lysate of a volume equivalent to that of a single individual. The abundance of endogenously produced DsRed2-OX5034 was determined by simultaneous probing of known quantities of a recombinant protein standard, followed by densitometric analysis of the protein bands and normalization of these bands to a housekeeping protein. DsRed2-OX5034 protein abundance is summarized in Table 1. These values may overestimate the DsRed2-OX5034 abundance because the antibody also recognized one or more endogenous proteins of similar molecular weight in the non-transgenic LWT strain, i.e., the value may represent the sum of DsRed2-OX5034 and one or more endogenous proteins. The relative protein abundance in the different mosquito life stages may be attributed to an increase in DsRed2-OX5034 protein abundance in adult mosquitoes compared to the pupal and larval stages and/or it may be the result of increased DsRed2-OX5034 expression (Unit II.A.1.). Total protein abundance in the mosquito lysates was not provided.

Table 1. Mean expression levels of DsRed2-OX5034 in various life stages of male OX5034 *Ae. aegypti*. ND = not detectable.

OX5034 life stage	Zygosity	DsRed2-OX5034 ng/ mosquito (volume lysate)
L4 larvae	Homozygous	7.7 ± 2.4
	Hemizygous	ND
Pupae	Homozygous	7.9 ± 0.4
	Hemizygous	ND
Adults 1-day post eclosion	Homozygous	ND
Adults 6-day post eclosion		35.3 ± 6.5

b. tTAV-OX5034

tTAV-OX5034 protein abundance was determined in the lysate of homo- and hemizygous OX5034 males at the larval, pupal, and two adult life stages. Mosquitoes were reared in the absence of tetracyclines, which means that protein abundance in these individuals is expected to be representative of those levels found in OX5034 males in the environment. A VP16 primary antibody was used to detect tTAV-OX5034 protein in these samples. The VP16 domain is part of the tTAV portion of tTAV-OX5034, which means that the primary antibody used in this assay is expected to recognize all three variations of the tTAV-OX5034 protein (full-length, cleaved, and dimerized).

A single band likely representing the monomeric tTAV variant was detected in lysate of homozygous adult OX5034 males at 1- and 6-days post eclosion. No tTAV-associated bands were identified in any of the immature life stages. The lysate of the adult life stages was simultaneously probed with a second primary antibody that recognized the housekeeping protein Hsp70, which was used to normalize the band intensity of the target protein (tTAV-OX5034). However, because the molecular weight of the Hsp70 protein is indistinguishable from both the full-length tTAV-OX5034 protein and the dimeric tTAV, it is possible that the Hsp70 protein band obfuscated the presence of these variants in the OX5034 lysate. As a result, the sum of tTAV-OX5034 associated proteins may have been underestimated. To account for that possibility, a conservative approach was taken in which it was assumed that the Hsp70-associated protein band in OX5034 homozygous adult males solely consists of tTAV-OX5034 and dimeric tTAV. That value was then added to that determined for the monomeric tTAV to result in the values presented in Table 2. It should be noted that a different housekeeping protein (GAPDH) was probed for in the immature life stages. GAPDH has a molecular weight that is distinguishable from all three tTAV-OX5034 protein variations.

Table 2. Mean expression levels of tTAV-OX5034 in various life stages of male OX5034 *Ae. aegypti*. ND = not detectable.

OX5034 life stage	Zygosity	tTAV-OX5034 ng/ mosquito (volume lysate)
L4 larvae	Homozygous	ND
	Hemizygous	ND
Pupae	Homozygous	ND
	Hemizygous	ND
Adults 1-day post eclosion	Homozygous	3.3 ± 0.3 ng
Adults 6-day post eclosion		2.2 ± 0.2 ng

c. Protein susceptibility to environmental proteases

tTAV-OX5034 and DsRed2-OX5034 are proteins and as such susceptible to the biotic processes of degradation in the environment through microbial activity. To further characterize protein behavior under these conditions and to gain insight into how long they may persist in the environment, susceptibility of tTAV-OX5034 and DsRed2-OX5034 to two environmental proteases was assessed. Two appropriate microbial proteases were chosen for this assessment: the serine proteases proteinase K and subtilisin A. Proteinase K was originally identified in the fungus *Tritirachium album* and subtilisins are produced by several *Bacillus* species [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Bioinformatic programs were used to predict the presence of proteolytic cleavage sites in the tTAV-OX5034 and DsRed2-OX5034 protein sequences. Secondly, an *in vitro* time-course assay was conducted on recombinant protein, using HN-tagged tTAV (as expressed in OX513A) and DsRed2 (Clontech) as proxies for the two OX5034-expressed proteins.

In silico analyses were computed using the Expert Protein Analysis System (ExPASy; Swiss Institute of Bioinformatics) PeptideCutter tool [ADDIN EN.CITE ADDIN EN.CITE.DATA]. The protein sequences of the full-length tTAV-OX5034 protein, the monomeric form tTAV, and DsRed2-OX5034 demonstrate that these proteins contain several predicted cleavage sites for proteinase K, indicating that they would be susceptible to its proteolytic activity. PeptideCutter does not include the option to predict the presence of subtilisin A cleavage sites and no such information was provided for tTAV-OX5034 and DsRed2-OX5034. The *in vitro* assays confirmed the *in silico* predicted susceptibility of tTAV (monomeric) to proteinase K, which was shown to be degraded at 37 °C within minutes. The remaining *in vitro* studies that investigated the susceptibility of tTAV-OX5034 and DsRed2-OX5034 to environmental proteases were inconclusive, for various reasons, including potential autolysis of proteinase K and subtilisin A. In addition, the lack of protein quantification hindered the determination of kinetics of these reactions.

There is no indication from the bioinformatics analyses, the *in vitro* data presented on tTAV, and general knowledge of proteins to suggest that tTAV-OX5034 and DsRed2-OX5034 would not be susceptible to degradation in the environment, especially given that microbially produced proteases are not limited to proteinase K and subtilisin A in the environment. However, further analysis is necessary to determine the kinetics of such degradation under environmental conditions.

5. Characterization of the OX5034 EP

a. Insecticide susceptibility

The OX5034 strain was tested for its susceptibility to several insecticides including the larvicide temephos (organophosphate) and the four adulticides permethrin (pyrethroid), deltamethrin (pyrethroid), malathion (organophosphate), and propoxur (carbamate). The insecticide susceptibility studies presented in MRIDs 50698718 and 50973405 are based on the standardized WHO threshold assays for the detection of insecticide resistance in *Ae. aegypti* (Temephos) and anopheline mosquitoes (four adulticides) at a single discriminating dose that is specific to each pesticide active ingredient [ADDIN EN.CITE <EndNote><Cite><Author>WHO</Author><Year>2016</Year><RecNum>279</RecNum><DisplayText>(WHO 2016, 2018)</DisplayText><record><rec-number>279</rec-number><foreign-keys><key app="EN" db-id="2t2pdevxize0spe5fsvxssfflfd5zwa2ex2s5" timestamp="1586878864">279</key></foreign-keys><ref-type name="Report">27</ref-type><contributors><authors><author>WHO</author></authors></contributors><titles><title>Monitoring and managing insecticide resistance in Aedes mosquito populations. Interim guidance for entomologists.</title></titles><dates><year>2016</year></dates><pub-location>https://apps.who.int/iris/handle/10665/204588</pub-

location><urls></urls></record></Cite><Cite><Author>WHO</Author><Year>2018</Year><RecNum>280</RecNum><record><rec-number>280</rec-number><foreign-keys><key app="EN" db-id="2t2pdevxize0spe5fsvxsfflfd5zwa2ex2s5" timestamp="1586878931">280</key></foreign-keys><ref-type name="Magazine Article">19</ref-type><contributors><authors><author>WHO</author></authors></contributors><titles><title>Test procedures for insecticide resistance monitoring in malaria vector mosquitoes. Second Edition. Updated June, 2018.</title></titles><dates><year>2018</year></dates><pub-location>https://apps.who.int/iris/bitstream/handle/10665/250677/9789241511575-eng.pdf;jsessionid=FA1AC3517A5FF22AF467FFBB71133981?sequence=1</pub-location><urls></urls></record></Cite></EndNote>]. These assays allow for the determination of potential resistance of a tested mosquito strain to the active ingredient through observation of mortality, but do not provide quantitative measures of resistance. Temephos susceptibility was furthermore investigated by determining the LC₅₀ for OX5034 and related strains.

In these WHO assays OX5034 was demonstrated to be susceptible to temephos, permethrin, deltamethrin, and malathion. After initially determining that the OX5034 strain was resistant to temephos at the WHO recommended discriminating dose, Oxitec repeated the study and showed that OX5034, OX513A, and the LWT strain are susceptible to the larvicide. The company furthermore determined the LC₅₀ for all three strains. The LC₅₀ of the two transgenic strains was somewhat lower than that of the LWT, but the values between the three strains were overall still comparable. OX5034, OX513A, and the LWT are expected to respond to temephos challenge in a comparable manner as these mosquitoes share much of the same genetic background. Given that the two transgenic strains are more closely related to the LWT than they are to each other and therefore it is possible that the somewhat lower LC₅₀ is a function of the transgenic traits imposing a fitness cost.

Genetic analysis of the OX5034 strain further support the results of the insecticide challenge that indicate that the OX5034 strain is susceptible to pyrethroids. Pyrethroid resistance in *Ae. aegypti* is often correlated with the presence of two single nucleotide polymorphisms (SNPs) in the Voltage-gated sodium channel gene (*VGSC*) that lead to two single amino acid substitutions, V1016I and F1534C, respectively [ADDIN EN.CITE ADDIN EN.CITE.DATA]. These mutations manifest in the so-called knockdown resistance (*kdr*) phenotype by reducing binding of the pyrethroids to the VGSC protein (reviewed in Hemingway and Ranson, 2000). Multiplex PCR analysis of *VGSC* demonstrated the absence of these resistance-associated alleles in OX5034. In *Ae. aegypti*, only one additional polymorphism, V410L has been associated with pyrethroid resistance. However, the two polymorphisms appear to have strong linkage [ADDIN EN.CITE ADDIN EN.CITE.DATA].

The information presented in the four MRIDs were acceptable to address the insecticide susceptibility of the OX5034 *Ae. aegypti* strain (Table 3). OX5034 was shown to be susceptible to the pesticide active ingredients temephos, permethrin, deltamethrin, and malathion and the strain does not carry pyrethroid resistance-associated *kdr* mutations. Thus, it is expected that these four insecticides are effective for controlling OX5034 in the field. While OX5034 showed possible resistance to propoxur, this adulticide active ingredient has not been registered for use on mosquitoes in the US since the late 1980s, when EPA determined that several outdoor uses of this chemical, including uses on mosquitoes, were not supported by the data [ADDIN EN.CITE

<EndNote><Cite><Author>EPA</Author><Year>1997</Year><RecNum>278</RecNum><DisplayText>(USEPA 1997)</DisplayText><record><rec-number>278</rec-number><foreign-keys><key app="EN" db-id="2t2pdevxize0spe5fsvxsfflfd5zwa2ex2s5" timestamp="1586878618">278</key></foreign-keys><ref-type name="Government Document">46</ref-

type><contributors><authors><author>USEPA</author></authors></contributors><titles><title>Reregistration Eligibility Decision (RED) - Propoxur.</title></titles><dates><year>1997</year></dates><work-type>Reregistration Eligibility Decision (RED)</work-type><urls></urls></record></Cite></EndNote>]. Thus, any resistance associated with propoxur will not affect current mosquito control practices.

b. Laboratory colony and arboviruses

As part of the proposed EUP, life male *Ae. aegypti* mosquitoes will be released into the environment. Like many other mosquito species, *Ae. aegypti* is a vector of arthropod-borne human illnesses. Arthropod-borne viruses (arboviruses) may be transmitted to humans through infected females during blood-feeding. Thus, the likelihood of introducing arboviruses into the environment through OX5034 field releases was evaluated.

Arboviruses are the causal agent of significant human disease nearly worldwide [ADDIN EN.CITE <EndNote><Cite><Author>Weaver</Author><Year>2010</Year><RecNum>520</RecNum><DisplayText>(Weaver and Reisen 2010)</DisplayText><record><rec-number>520</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586881596">520</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Weaver, S. C.</author><author>Reisen, W. K.</author></authors></contributors><titles><title>Present and future arboviral threats</title><secondary-title>Antiviral Research</secondary-title></titles><periodical><full-title>Antiviral Research</full-title></periodical><pages>328-345</pages><volume>85</volume><number>2</number><dates><year>2010</year><pub-dates><date>Feb</date></pub-dates></dates><isbn>0166-3542</isbn><accession-num>WOS:000274748900002</accession-num><urls><related-urls><url><Go to ISI>://WOS:000274748900002</url></related-urls></urls><electronic-resource-num>10.1016/j.antiviral.2009.10.008</electronic-resource-num></record></Cite></EndNote>]. *Ae. aegypti* is commonly recognized as the principal vector of the yellow fever virus (YFV), dengue viruses (DENV-1, DENV-2, DENV-3, DENV-4), chikungunya virus (CHIKV), and Zika viruses (ZIKV) [ADDIN EN.CITE <EndNote><Cite><Author>Souza-Neto</Author><Year>2019</Year><RecNum>277</RecNum><DisplayText>(Souza-Neto et al. 2019)</DisplayText><record><rec-number>277</rec-number><foreign-keys><key app="EN" db-id="2t2pdevxize0spe5fsvxsf1fd5zwa2ex2s5" timestamp="1586878193">277</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Souza-Neto, J. A.</author><author>Powell, J. R.</author><author>Bonizzoni, M.</author></authors></contributors><auth-address>Sao Paulo State University (UNESP), School of Agricultural Sciences, Department of Bioprocesses and Biotechnology, Multiuser Central Laboratory, Botucatu, Brazil; Sao Paulo State University (UNESP), Institute of Biotechnology, Botucatu, Brazil.Yale University, New Haven, CT, USA.Department of Biology and Biotechnology, University of Pavia, Pavia, Italy. Electronic address: m.bonizzoni@unipv.it.</auth-address><titles><title>*Aedes aegypti* vector competence studies: A review</title><secondary-title>Infect Genet Evol</secondary-title></titles><periodical><full-title>Infect Genet Evol</full-title></periodical><pages>191-209</pages><volume>67</volume><edition>2018/11/23</edition><keywords><keyword>*Aedes*/*genetics/*virology</keyword><keyword>Animals</keyword><keyword>*Genetic Variation</keyword><keyword>*Host-Pathogen Interactions</keyword><keyword>Humans</keyword><keyword>Microbiota</keyword><keyword>Mosquito Vectors/*genetics/*virology</keyword><keyword>Virus

Diseases/*transmission/virology</keyword></keywords><dates><year>2019</year><pub-dates><date>Jan</date></pub-dates></dates><isbn>1567-7257 (Electronic)1567-1348 (Linking)</isbn><accession-num>30465912</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/30465912</url></related-urls></urls><electronic-resource-num>10.1016/j.meegid.2018.11.009</electronic-resource-num></record></Cite></EndNote>]. While some studies have demonstrated that *Ae. aegypti* can itself be infected with other arboviruses that are of human health significance, transmission to other hosts, such as humans and wildlife, was found to be unlikely. Amongst those are the West Nile virus (WNV), the Sindbis virus (SINV), and Mayaro virus (MAYV). In laboratory studies that examined the impact of *Wolbachia* on the replication of WNV it was demonstrated that while *Ae. aegypti* can be experimentally infected with WNV, however, no infectious virus was detected in saliva from these mosquitoes [ADDIN EN.CITE <EndNote><Cite><Author>Joubert</Author><Year>2017</Year><RecNum>517</RecNum><DisplayText>(Joubert and O'Neill 2017)</DisplayText><record><rec-number>517</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586881596">517</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Joubert, D. A.</author><author>O'Neill, S. L.</author></authors></contributors><titles><title>Comparison of Stable and Transient *Wolbachia* Infection Models in *Aedes aegypti* to Block Dengue and West Nile Viruses</title><secondary-title>Plos Neglected Tropical Diseases</secondary-title></titles><periodical><full-title>Plos Neglected Tropical Diseases</full-title></periodical><volume>11</volume><number>1</number><dates><year>2017</year><pub-dates><date>Jan</date></pub-dates></dates><isbn>1935-2735</isbn><accession-num>WOS:000394152000047</accession-num><urls><related-urls><url><Go to ISI>://WOS:000394152000047</url></related-urls></urls><custom7>e0005275</custom7><electronic-resource-num>10.1371/journal.pntd.0005275</electronic-resource-num></record></Cite></EndNote>]. The major vectors of WNV are found within the genus *Culex*, including *Cx. pipiens*, *Cx. tarsalis*, *Cx. modestus*, and *Cx. quinquefasciatus* [ADDIN EN.CITE <EndNote><Cite><Author>Chapman</Author><Year>2018</Year><RecNum>515</RecNum><DisplayText>(Chapman et al. 2018)</DisplayText><record><rec-number>515</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586881596">515</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Chapman, G. E.</author><author>Baylis, M.</author><author>Archer, D.</author><author>Daly, J. M.</author></authors></contributors><titles><title>The challenges posed by equine arboviruses</title><secondary-title>Equine Veterinary Journal</secondary-title></titles><periodical><full-title>Equine Veterinary Journal</full-title></periodical><pages>436-445</pages><volume>50</volume><number>4</number><dates><year>2018</year><pub-dates><date>Jul</date></pub-dates></dates><isbn>0425-1644</isbn><accession-num>WOS:000434413100003</accession-num><urls><related-urls><url><Go to ISI>://WOS:000434413100003</url></related-urls></urls><electronic-resource-num>10.1111/evj.12829</electronic-resource-num></record></Cite></EndNote>]. Experimental evidence of *Ae. aegypti* infection with MAYV exists, but no wild transmission of MAYV by *Ae. aegypti* has been reported to date [ADDIN EN.CITE <EndNote><Cite><Author>Pezzi</Author><Year>2020</Year><RecNum>521</RecNum><DisplayText>(Pezzi et al. 2020)</DisplayText><record><rec-number>521</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5"

timestamp="1586883176">521</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Pezzi, L.</author><author>M. Diallo</author><author>M.G. Rosa-Freitas</author><author>A. Vega-Rua</author><author>L.F.P. Ng</author><author>S. Boyer</author><author>J.F. Drexler</author><author>N. Vasilakis</author><author>R. Lourenco-de-Oliveira</author><author>S.C. Weaver</author><author>A. Kohl</author><author>X. de Lamballerie</author><author>A.-B. Failloux</author><author>P. Brasil</author><author>M. Busch</author><author>M.S. Diamond</author><author>M.A. Drebot</author><author>P. Gallian</author><author>T. Jaenisch</author><author>A.D. LaBeaud</author><author>M. Lecuit</author><author>J. Neyts</author><author>C.B. Reusken</author><author>G.S. Ribeiro</author><author>M. Rios</author><author>A.J. Rodriguez-Morales</author><author>A. Sall</author><author>G. Simmons</author><author>F. Simon</author><author>A.M. Siqueira</author></authors></contributors><titles><title>GloPID-R report on chikungunya, o'nyong-nyong and Mayaro virus, part 5: Entomological aspects</title><secondary-title>Antiviral Research</secondary-title></titles><periodical><full-title>Antiviral Research</full-title></periodical><volume>174</volume><dates><year>2020</year></dates><urls></urls><electronic-resource-num>https://doi.org/10.1016/j.antiviral.2019.104670.</electronic-resource-num></record></Cite></EndNote>]. [ADDIN EN.CITE <EndNote><Cite AuthorYear="1"><Author>Serra</Author><Year>2016</Year><RecNum>518</RecNum><DisplayText>Serra et al. (2016)</DisplayText><record><rec-number>518</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586881596">518</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Serra, O. P.</author><author>Cardoso, B. F.</author><author>Ribeiro, A. L. M.</author><author>dos Santos, F. A. L.</author><author>Slhessarenko, R. D.</author></authors></contributors><titles><title>Mayaro virus and dengue virus 1 and 4 natural infection in culicids from Cuiaba, state of Mato Grosso, Brazil</title><secondary-title>Memorias Do Instituto Oswaldo Cruz</secondary-title></titles><periodical><full-title>Memorias Do Instituto Oswaldo Cruz</full-title></periodical><pages>20-29</pages><volume>111</volume><number>1</number><dates><year>2016</year><pub-dates><date>Jan</date></pub-dates></dates><isbn>0074-0276</isbn><accession-num>WOS:000369240000002</accession-num><urls><related-urls><url><Go to ISI>://WOS:000369240000002</url></related-urls></urls><electronic-resource-num>10.1590/0074-02760150270</electronic-resource-num></record></Cite></EndNote>], found non-engorged *Ae. aegypti* naturally infected with MAYV in the city of Cuiab  (Brazil), however either no or poor infection and dissemination rates were demonstrated when orally challenged with artificial blood meals containing MAYV at titers similar to those usually found in infected humans [ADDIN EN.CITE ADDIN EN.CITE.DATA], which may limit chances to initiate an urban transmission cycle. In laboratory conditions, two strains of *Ae. aegypti* from Florida and Iquitos (Peru) were competent to transmit MAYV [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Major vectors of the MAYV includes mosquito species of the genus *Haemagogus*. Major vectors for SINV include *Culex spp.* and *Culiseta spp.* [ADDIN EN.CITE <EndNote><Cite><Author>Chapman</Author><Year>2018</Year><RecNum>515</RecNum><DisplayText>(Chapman et al. 2018)</DisplayText><record><rec-number>515</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586881596">515</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Chapman, G. E.</author><author>Baylis, M.</author><author>Archer, D.</author><author>Daly, J.

M. </author></authors></contributors><titles><title>The challenges posed by equine arboviruses</title><secondary-title>Equine Veterinary Journal</secondary-title></titles><periodical><full-title>Equine Veterinary Journal</full-title></periodical><pages>436-445</pages><volume>50</volume><number>4</number><dates><year>2018</year><pub-dates><date>Jul</date></pub-dates></dates><isbn>0425-1644</isbn><accession-num>WOS:000434413100003</accession-num><urls><related-urls><url><Go to ISI>://WOS:000434413100003</url></related-urls></urls><electronic-resource-num>10.1111/evj.12829</electronic-resource-num></record></Cite></EndNote>]. A laboratory study conducted by [ADDIN EN.CITE <EndNote><Cite AuthorYear="1"><Author>Muturi</Author><Year>2011</Year><RecNum>522</RecNum><DisplayText>Muturi et al. (2011)</DisplayText><record><rec-number>522</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586883567">522</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Muturi, E. J.</author><author>Kim, C. H.</author><author>Alto, B. W.</author><author>Berenbaum, M. R.</author><author>Schuler, M. A.</author></authors></contributors><titles><title>Larval environmental stress alters *Aedes aegypti* competence for Sindbis virus</title><secondary-title>Tropical Medicine & International Health</secondary-title></titles><periodical><full-title>Tropical Medicine & International Health</full-title></periodical><pages>955-964</pages><volume>16</volume><number>8</number><dates><year>2011</year><pub-dates><date>Aug</date></pub-dates></dates><isbn>1360-2276</isbn><accession-num>WOS:000292647200007</accession-num><urls><related-urls><url><Go to ISI>://WOS:000292647200007</url></related-urls></urls><electronic-resource-num>10.1111/j.1365-3156.2011.02796.x</electronic-resource-num></record></Cite></EndNote>] used *Ae. aegypti* to examine the effect of larval stress on vector competence for SINV and found that stress during larval development may cause alterations in adult mosquito phenotype and immunity that can increase their susceptibility to pathogens. This study demonstrates that *Ae. aegypti* can be experimentally infected with SINV in the laboratory.

OX5034 *Ae. aegypti* has been maintained as a laboratory colony since it was developed in 2006. Infection of the colony under these controlled conditions is unlikely to occur. The most probable entry of arboviruses can be envisioned through infected blood fed to females as part of their normal diet. The horse blood used in the female diet is sold for use in molecular research, certified free of bacteria and certain equine viruses (MRID 508894-27). The donor horses are permanent residents on a farm located in the UK and are under veterinary care. Importantly, neither invasive *Ae. aegypti*, nor relevant arboviruses are endemic to the UK, and thus it is unlikely that these arboviruses would be present in the OX5034 colony.

Ae. aegypti is found in tropical and sub-tropical regions where it is the major vector of DENV, YFV, CHIKV and, more recently, ZIKV. Given the importance of *Ae. aegypti* as a vector of arboviruses and its propensity to be transported to new regions, the European Centre for Disease Prevention and Control (ECDC) has placed *Ae. aegypti* on a list of potentially invasive mosquito species. *Ae. aegypti* is found in some European countries, such as the Netherlands (not established) and the archipelago of Madeira, as well as southern Russia, Georgia and Turkey [ADDIN EN.CITE <EndNote><Cite><Author>Dallimore</Author><Year>2017</Year><RecNum>516</RecNum><DisplayText>(Dallimore et al. 2017)</DisplayText><record><rec-number>516</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586881596">516</key></foreign-keys><ref-type name="Journal Article">17</ref-

type><contributors><authors><author>Dallimore, T.</author><author>Hunter, T.</author><author>Medlock, J. M.</author><author>Vaux, A. G. C.</author><author>Harbach, R. E.</author><author>Strode, C.</author></authors></contributors><titles><title>Discovery of a single male *Aedes aegypti* (L.) in Merseyside, England</title><secondary-title>Parasites & Vectors</secondary-title></titles><periodical><full-title>Parasites & Vectors</full-title></periodical><volume>10</volume><dates><year>2017</year><pub-dates><date>Jun</date></pub-dates></dates><isbn>1756-3305</isbn><accession-num>WOS:000404074500006</accession-num><urls><related-urls><url><Go to ISI>://WOS:000404074500006</url></related-urls></urls><custom7>309</custom7><electronic-resource-num>10.1186/s13071-017-2251-0</electronic-resource-num></record></Cite></EndNote>]. Public Health England (PHE) runs a nationwide mosquito surveillance project which conducts surveys for invasive mosquitoes in the UK, including *Aedes* spp. at ports of entry since 2011 [ADDIN EN.CITE ADDIN EN.CITE.DATA]. While these surveillance efforts have on occasion recorded the presence of few *Aedes* individuals, the UK currently has no known established populations of any invasive *Aedes* spp. mosquitoes [ADDIN EN.CITE <EndNote><Cite><Author>Medlock</Author><Year>2018</Year><RecNum>514</RecNum><DisplayText>(Medlock et al. 2018)</DisplayText><record><rec-number>514</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586881596">514</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Medlock, J. M.</author><author>Hansford, K. M.</author><author>Vaux, A. G. C.</author><author>Cull, B.</author><author>Gillingham, E.</author><author>Leach, S.</author></authors></contributors><titles><title>Assessment of the Public Health Threats Posed by Vector-Borne Disease in the United Kingdom (UK)</title><secondary-title>International Journal of Environmental Research and Public Health</secondary-title></titles><periodical><full-title>International Journal of Environmental Research and Public Health</full-title></periodical><volume>15</volume><number>10</number><dates><year>2018</year><pub-dates><date>Oct</date></pub-dates></dates><isbn>1660-4601</isbn><accession-num>WOS:000448818100087</accession-num><urls><related-urls><url><Go to ISI>://WOS:000448818100087</url></related-urls></urls><custom7>2145</custom7><electronic-resource-num>10.3390/ijerph15102145</electronic-resource-num></record></Cite></EndNote>]. For example, in 2014, a single male *Ae. aegypti* was found in Merseyside, North West England, however follow-up surveys determined that there was no established population [ADDIN EN.CITE <EndNote><Cite><Author>Dallimore</Author><Year>2017</Year><RecNum>516</RecNum><DisplayText>(Dallimore et al. 2017)</DisplayText><record><rec-number>516</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586881596">516</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Dallimore, T.</author><author>Hunter, T.</author><author>Medlock, J. M.</author><author>Vaux, A. G. C.</author><author>Harbach, R. E.</author><author>Strode, C.</author></authors></contributors><titles><title>Discovery of a single male *Aedes aegypti* (L.) in Merseyside, England</title><secondary-title>Parasites & Vectors</secondary-title></titles><periodical><full-title>Parasites & Vectors</full-title></periodical><volume>10</volume><dates><year>2017</year><pub-dates><date>Jun</date></pub-dates></dates><isbn>1756-3305</isbn><accession-num>WOS:000404074500006</accession-num><urls><related-urls><url><Go to ISI>://WOS:000404074500006</url></related-urls></urls><custom7>309</custom7><electronic-resource-num>10.1186/s13071-017-2251-0</electronic-resource-num></record></Cite></EndNote>].

None of the arboviruses (DENV, YFV, CHIKV and ZIKV) for which *Ae. aegypti* is a major vector occur naturally in the UK. The most recent data in the ECDPC's Surveillance Atlas for Infectious Disease show no locally acquired cases of DENV, YFV, CHIKV and ZIKV in the UK [ADDIN EN.CITE <EndNote><Cite ExcludeAuth="1"><Author>European Centre for Disease Prevention and Control</Author><Year>2017</Year><RecNum>524</RecNum><Prefix>ECDPC</Prefix><DisplayText>(ECDPC 2017)</DisplayText><record><rec-number>524</rec-number><foreign-keys><key app="EN" db-id="9dafa52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586884104">524</key></foreign-keys><ref-type name="Web Page">12</ref-type><contributors><authors><author>European Centre for Disease Prevention and Control,</author></authors></contributors><titles><title>Surveillance Atlas for Infectious Disease</title></titles><number>Last Accessed April 8, 2020</number><dates><year>2017</year></dates><urls><related-urls><url><http://atlas.ecdc.europa.eu/public/index.aspx?Dataset=27&HealthTopic=16></url></related-urls></urls></record></Cite></EndNote>]. The only recorded cases were acquired while traveling outside of the country. In recent years a small number of travel-related Chikungunya cases have been reported in England, Wales and Northern Ireland on an annual basis. Most infections have been acquired while on travel in the Indian sub-continent and South East Asia. In 2014, 295 cases of Chikungunya were reported in England, Wales and Northern Ireland of which 88% had acquired their infection in the Caribbean and South America [ADDIN EN.CITE <EndNote><Cite><Author>Public Health England</Author><Year>2014</Year><RecNum>523</RecNum><DisplayText>(Public Health England 2014)</DisplayText><record><rec-number>523</rec-number><foreign-keys><key app="EN" db-id="9dafa52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586883937">523</key></foreign-keys><ref-type name="Web Page">12</ref-type><contributors><authors><author>Public Health England,</author></authors></contributors><titles><title>The characteristics, symptoms, diagnosis and epidemiology of chikungunya</title></titles><dates><year>2014</year></dates><urls><related-urls><url><https://www.gov.uk/guidance/chikungunya></url></related-urls></urls></record></Cite></EndNote>]. Cases of Dengue in UK travelers are increasing, with most reported in travelers who visited Asia, the Americas and the Caribbean [ADDIN EN.CITE <EndNote><Cite><Author>Public Health England</Author><Year>2014</Year><RecNum>523</RecNum><DisplayText>(Public Health England 2014)</DisplayText><record><rec-number>523</rec-number><foreign-keys><key app="EN" db-id="9dafa52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586883937">523</key></foreign-keys><ref-type name="Web Page">12</ref-type><contributors><authors><author>Public Health England,</author></authors></contributors><titles><title>The characteristics, symptoms, diagnosis and epidemiology of chikungunya</title></titles><dates><year>2014</year></dates><urls><related-urls><url><https://www.gov.uk/guidance/chikungunya></url></related-urls></urls></record></Cite></EndNote>]. In 2017, there were 465 cases of imported Dengue [ADDIN EN.CITE <EndNote><Cite ExcludeAuth="1"><Author>European Centre for Disease Prevention and Control</Author><Year>2017</Year><RecNum>524</RecNum><Prefix>ECDPC</Prefix><DisplayText>(ECDPC 2017)</DisplayText><record><rec-number>524</rec-number><foreign-keys><key app="EN" db-id="9dafa52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586884104">524</key></foreign-keys><ref-type name="Web Page">12</ref-type><contributors><authors><author>European Centre for Disease Prevention and Control,</author></authors></contributors><titles><title>Surveillance Atlas for Infectious Disease</title></titles><number>Last Accessed April 8, 2020</number><dates><year>2017</year></dates><urls><related-urls><url><http://atlas.ecdc.europa.eu/public/index.aspx?Dataset=27&HealthTopic=16></url></related-

d-urls></urls></record></Cite></EndNote>]. In 2019 the first case of locally acquired Zika was reported to have occurred in southern France [ADDIN EN.CITE <EndNote><Cite><Author>Brady</Author><Year>2019</Year><RecNum>527</RecNum><DisplayText>(Brady and Hay 2019)</DisplayText><record><rec-number>527</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586885888">527</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Brady, O. J.</author><author>Hay, S. I.</author></authors></contributors><titles><title>The first local cases of Zika virus in Europe</title><secondary-title>Lancet</secondary-title></titles><periodical><full-title>Lancet</full-title></periodical><pages>1991-1992</pages><volume>394</volume><number>10213</number><dates><year>2019</year><pub-dates><date>Nov</date></pub-dates></dates><isbn>0140-6736</isbn><accession-num>WOS:000500950200023</accession-num><urls><related-urls><url><Go to ISI>://WOS:000500950200023</url></related-urls></urls><electronic-resource-num>10.1016/s0140-6736(19)32790-4</electronic-resource-num></record></Cite></EndNote>], but no vector-borne locally acquired Zika cases were reported by EU/EEA countries in other part of Europe as of week 12, 2019 [ADDIN EN.CITE <EndNote><Cite ExcludeAuth="1"><Author>European Centre for Disease Prevention and Control</Author><Year>2019</Year><RecNum>525</RecNum><Prefix>ECDPC</Prefix><DisplayText>(ECDPC 2019)</DisplayText><record><rec-number>525</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586884152">525</key></foreign-keys><ref-type name="Web Page">12</ref-type><contributors><authors><author>European Centre for Disease Prevention and Control,</author></authors></contributors><titles><title>Zika virus transmission worldwide, Rapid Risk Assessment 9 April, 2019</title></titles><dates><year>2019</year></dates><urls><related-urls><url>https://www.ecdc.europa.eu/sites/default/files/documents/zika-risk-assessment-9-april-2019.pdf</url></related-urls></urls></record></Cite></EndNote>]. According to a risk assessment for ZIKV released in April, 2019 by the ECDPC, between 2015 and week 12 of 2019, 22 EU/EEA Member States reported 2,398 travel-associated ZIKV infections through the European Surveillance System. France reported 48% of the cases, Spain 15% and the UK, 9%. In 2017, the ECDPC reported one travel-related case of Yellow fever in the Netherlands [ADDIN EN.CITE <EndNote><Cite ExcludeAuth="1"><Author>European Centre for Disease Prevention and Control</Author><Year>2017</Year><RecNum>524</RecNum><Prefix>ECDPC</Prefix><DisplayText>(ECDPC 2017)</DisplayText><record><rec-number>524</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586884104">524</key></foreign-keys><ref-type name="Web Page">12</ref-type><contributors><authors><author>European Centre for Disease Prevention and Control,</author></authors></contributors><titles><title>Surveillance Atlas for Infectious Disease</title></titles><number>Last Accessed April 8, 2020</number><dates><year>2017</year></dates><urls><related-urls><url>http://atlas.ecdc.europa.eu/public/index.aspx?Dataset=27&HealthTopic=16</url></related-urls></urls></record></Cite></EndNote>].

The OX5034 *Ae. aegypti* colony is maintained under biological containment level 2 at Oxitec's insectary and the dietary horse blood is prepared by the vendor for microbiological use. Under these controlled rearing conditions, the likelihood for disease-causing agents to be introduced into the mosquito colony is low. Further, because neither *Ae. aegypti* nor arboviruses for which *Ae. aegypti* is a major vector have established in the UK, the presence of these arboviruses in the colony is equally unlikely. Consequently,

were the colony to be moved outside of the UK, or evidence becomes available of establishment of invasive *Aedes* or arboviruses for which *Ae. aegypti* is a principal vector, testing of the OX5034 colony for arbovirus presence will be required.

c. Fecundity

The OX5034 strain was evaluated for fecundity through an egg clutch analysis. Three experimental cages each contained 100 immature OX5034 homozygous males and 200 immature LWT females. One cage of 100 immature LWT males and 200 immature LWT females was set up as a control. The cages were left for 12 days to allow pupae to emerge as adults, mature and mate. Females were then blood fed twice over a three-day period. Two days after the second blood feeding, an oviposition substrate was provided and was then removed two days later. Egg collection happened over four gonotrophic cycles and oviposition papers from the 2nd and 3rd gonotrophic cycles were photographed and analyzed using ImageJ software to estimate total egg number.

The study found that OX5034 homozygous males mated to LWT females produced smaller egg clutch sizes than LWT males mated to LWT females over the two gonotrophic cycles assessed. Specifically, the study found for OX5034 homozygous males mated to LWT females, the average number of eggs from the 2nd gonotrophic cycle was 30 ± 4.7 eggs and 40 ± 11.1 eggs from the 3rd gonotrophic cycle. This was compared to LWT males mated to LWT females, where the average number of eggs from the 2nd gonotrophic cycle was 53 eggs and 54 eggs from the 3rd gonotrophic cycle. The smaller egg clutch sizes from OX5034 matings may indicate a fitness cost to the OX5034 transgene.

As the LWT strain was used to produce the OX5034 strain, EPA also evaluated how results from both laboratory matings compared to reports on wild *Ae. aegypti* clutch sizes in order to determine how the strain's background genetics may impact fecundity. The below values are from a literature search provided by Oxitec:

CDC National Center for Emerging and Zoonotic Infectious Diseases: 100 eggs/clutch
([HYPERLINK "<https://www.cdc.gov/dengue/resources/factSheets/MosquitoLifecycleFINAL.pdf>"])

Cold Spring Harbor Protocol [ADDIN EN.CITE

<EndNote><Cite><Author>Clemons</Author><Year>2010</Year><RecNum>481</RecNum><DisplayText>(Clemons et al. 2010)</DisplayText><record><rec-number>481</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1578060848">481</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Clemons, A.</author><author>Mori, A.</author><author>Haugen, M.</author><author>Severson, D.W.</author><author>Duman-Scheel, M.</author></authors></contributors><titles><title><style face="normal" font="default" size="100%">Culturing and egg collection of </style><style face="italic" font="default" size="100%">*Aedes aegypti*</style></title><secondary-title>Cold Spring Harbor Protocols</secondary-title></titles><periodical><full-title>Cold Spring Harbor Protocols</full-title></periodical><pages>pdb prot

5507</pages><volume>2010</volume><dates><year>2010</year></dates><urls></urls></record></Cite></EndNote>]: 100-150 eggs/clutch

Singapore National Environment Agency: 100 eggs/clutch
([HYPERLINK "<https://www.nea.gov.sg/dengue-zika/prevent-aedes-mosquito-breeding/aedes-mosquito>"])

Metabolic relationship between female body size, reserves and fecundity of Aedes aegypti [ADDIN EN.CITE

26-118 eggs/clutch

<EndNote><Cite><Author>Briegel</Author><Year>1990</Year><RecNum>479</RecNum><DisplayText>(Briegel 1990)</DisplayText><record><rec-number>479</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1578060419">479</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Briegel, H.</author></authors></contributors><titles><title><style face="normal" font="default" size="100%">Metabolic relationship between female body size, reserves, and fecundity of </style><style face="italic" font="default" size="100%">Aedes aegypti</style></title><secondary-title>Journal of Insect Physiology</secondary-title></titles><periodical><full-title>Journal of Insect Physiology</full-title></periodical><pages>165-172</pages><volume>36</volume><number>3</number><dates><year>1990</year></dates><isbn>0022-1910</isbn><accession-num>WOS:A1990CY23500004</accession-num><urls><related-urls><url><Go to ISI>;//WOS:A1990CY23500004</url></related-urls></urls><electronic-resource-num>10.1016/0022-1910(90)90118-y</electronic-resource-num></record></Cite></EndNote>];

The values provided above by the applicant are also in line with a literature search conducted by EPA [ADDIN EN.CITE ADDIN EN.CITE.DATA]. The clutch sizes of the LWT and OX5034 mosquito matings are within the range expected for *Ae. aegypti*.

d. Longevity

The longevity of OX5034 mosquitoes was also evaluated both with and without a tetracycline analogue dietary antidote and the results were compared against LWT mosquitoes. OX5034 males (homozygous and hemizygous), OX5034 homozygous females, and LWT were reared and mated for two days prior to being isolated for longevity analysis. All adults were provided with 10% sucrose solution *ad libitum* and females received two blood meals (day 7 and 17). To determine longevity, dead adults from all cages were removed daily and counted.

When reared with the dietary antidote, OX5034 homozygous females have lower longevity than LWT females. Specifically, OX5034 homozygous female mosquitoes and LWT female mosquitoes were found to have median survivals of 42 days and 56 days, respectively. When reared without the dietary antidote, the study found similar longevity between OX5034 hemizygous males with median survival of 44 days and LWT males with median survival of 50 days. Conversely, the study found reduced longevity in OX5034 homozygous males with a median survival of 24 days compared to LWT males with a median survival of 49 days. The reduced longevity of OX5034 homozygous males may indicate a fitness cost to the OX5034 transgene, but that cost is likely related to the number of transgene copies, as the OX5034 hemizygous males did not show reduced longevity.

As the LWT strain was used to produce the OX5034 strain, EPA also evaluated how results from both LWT and OX5034 analyses compared to reports on wild *Ae. aegypti* longevity in order to determine how the strain's background genetics may impact lifespan. A literature search indicates that median survival rates reported by the applicant are within the range reported in similar lab studies measuring *Ae. aegypti* longevity when provided with food sources:

Superior reproductive success on human blood without sugar is not limited to highly anthropophilic mosquito species [ADDIN EN.CITE

<EndNote><Cite><Author>Braks</Author><Year>2006</Year><RecNum>483</RecNum><DisplayText>(Braks et al. 2006)</DisplayText><record><rec-number>483</rec-number><foreign-keys><key

app="EN" db-id="9dafa52dcp9s9xe99drvp0fnwz0sz59xdwa5"
 timestamp="1578067263">483</key></foreign-keys><ref-type name="Journal Article">17</ref-
 type><contributors><authors><author>Braks, M. A. H.</author><author>Juliano, S.
 A.</author><author>Lounibos, L. P.</author></authors></contributors><titles><title>Superior
 reproductive success on human blood without sugar is not limited to highly anthropophilic mosquito
 species</title><secondary-title>Medical and Veterinary Entomology</secondary-
 title></titles><periodical><full-title>Medical and Veterinary Entomology</full-
 title></periodical><pages>53-
 59</pages><volume>20</volume><number>1</number><dates><year>2006</year><pub-
 dates><date>Mar</date></pub-dates></dates><isbn>0269-283X</isbn><accession-
 num>WOS:000236174700006</accession-num><urls><related-urls><url><Go to
 ISI>://WOS:000236174700006</url></related-urls></urls><electronic-resource-
 num>10.1111/j.1365-2915.2006.00612.x</electronic-resource-num></record></Cite></EndNote>]:

57.18 ± 4.26 days, female, sugar + blood meal

38.09 ± 7.09 days, female, blood meal

*Parity and longevity of Aedes aegypti According to temperatures in controlled conditions and
 consequences on dengue transmission risks* [ADDIN EN.CITE
 <EndNote><Cite><Author>Goindin</Author><Year>2015</Year><RecNum>476</RecNum><Display
 Text>(Goindin et al. 2015)</DisplayText><record><rec-number>476</rec-number><foreign-keys><key
 app="EN" db-id="9dafa52dcp9s9xe99drvp0fnwz0sz59xdwa5"
 timestamp="1578060419">476</key></foreign-keys><ref-type name="Journal Article">17</ref-
 type><contributors><authors><author>Goindin, D.</author><author>Delannay,
 C.</author><author>Ramdini, C.</author><author>Gustave, J.</author><author>Fouque,
 F.</author></authors></contributors><titles><title>Parity and Longevity of Aedes aegypti According to
 Temperatures in Controlled Conditions and Consequences on Dengue Transmission
 Risks</title><secondary-title>Plos One</secondary-title></titles><periodical><full-title>Plos One</full-
 title></periodical><volume>10</volume><number>8</number><dates><year>2015</year><pub-
 dates><date>Aug</date></pub-dates></dates><isbn>1932-6203</isbn><accession-
 num>WOS:000359352600069</accession-num><urls><related-urls><url><Go to
 ISI>://WOS:000359352600069</url></related-
 urls></urls><custom7>e0135489</custom7><electronic-resource-
 num>10.1371/journal.pone.0135489</electronic-resource-num></record></Cite></EndNote>]:

9-51 days, female, sugar + blood meal, 24 °C

14-56 days, female, sugar + blood meal, 27 °C

19-40 days, female, sugar + blood meal, 30 °C

The adaptation of field collected Aedes aegypti (L.) and Aedes albopictus (Skuse) in laboratory conditions
 [ADDIN EN.CITE
 <EndNote><Cite><Author>Manorenjitha</Author><Year>2015</Year><RecNum>482</RecNum><Di
 splayText>(Manorenjitha and Zairi 2015)</DisplayText><record><rec-number>482</rec-
 number><foreign-keys><key app="EN" db-id="9dafa52dcp9s9xe99drvp0fnwz0sz59xdwa5"
 timestamp="1578066051">482</key></foreign-keys><ref-type name="Journal Article">17</ref-
 type><contributors><authors><author>Manorenjitha, M.S.</author><author>Zairi,
 J.</author></authors></contributors><titles><title><style face="normal" font="default"
 size="100%">The adaptation of field collected </style><style face="italic" font="default"

size="100%">*Aedes aegypti*</style><style face="normal" font="default" size="100%"> (L.) and
</style><style face="italic" font="default" size="100%">*Aedes albopictus*</style><style face="normal"
font="default" size="100%"> (Skuse) in laboratory condition</style></title><secondary-
title>International Journal of Life Science and Medical Research</secondary-
title></titles><periodical><full-title>International Journal of Life Science and Medical Research</full-
title></periodical><pages>25-
30</pages><volume>5</volume><number>4</number><dates><year>2015</year></dates><urls></urls
></record></Cite></EndNote>]:

51.7 ± 1.22 days, male, sugar
51.7 ± 1.31 days, female, sugar
45.1 ± 1.25 days, female, sugar + blood meal

The longevity of the LWT strain mosquitoes and the OX5034 mosquitoes are within the range expected for *Ae. aegypti*.

6. Analytical detection methods

Information was provided that showed that field-collected hemizygous OX5034 *Ae. aegypti* larvae expressing the DsRed2-OX5034 fluorescent protein can be visually identified using the fluorescence screening protocol. The current enforcement analytical method has been demonstrated to be a reliable qualitative indicator of DsRed2-OX5034 presence, e.g., determination of OX5034 inheritance pattern in Unit IV.5. To account for those instances in which larvae may exhibit an ambiguous pattern of fluorescence, the reviewer recommends that the more sensitive PCR-based methods for identification of the OX5034 genetic construct, cited in the experimental protocol in section 5.2.6.1, should be made available as an alternative enforcement analytical method. The PCR protocol is described in detail in MRID 50889427 in SOPs QD-R-00109 and QD-R-00108.

Table 3. Classification of the data submitted for the product characterization and manufacturing process of OX5034 *Ae. aegypti*.

Study type/ Title	OPPTS Guideline No.	Results Summary and Classification	MRID No.
Manufacturing process	880.1200	The information contained in this MRID describes the production and quality assurance processes used in the development and manufacture of the OX5034 <i>Ae. aegypti</i> mosquitoes. The plasmid map detailing the genetic elements, the procedures for microinjection, and the identification of transformants are appropriately detailed as part of the production of the end-use product, the OX5034 male mosquitoes. A thorough screening process with selective criteria and the demonstration that no females are produced (in the absence of tetracyclines) regardless of zygosity is critical and described in detail. The procedures and quality assurance protocols described in this MRID are acceptable for these purposes. Classification: Acceptable.	50889424
Standard Operating Procedures for Production of <i>Aedes aegypti</i> OX5034	880.1200	The information contained in this MRID details the protocols for production and quality assurance of male mosquitoes for release to the environment. Descriptions of egg, larval, pupal and adult mosquito production included are scientifically sound and the attention to quality	50889427

		assurance / quality control, certification of technical support staff, and record keeping are scientifically sound and based upon accepted methodologies. A description of sexing protocols and enumeration of larvae, pupae and adults are discussed. The study is acceptable for use in production of OX5034. Classification: Acceptable.	
OX5034 <i>Aedes aegypti</i> : Product Identity and Composition, Discussion of the Formation of Impurities, Preliminary Analysis, Certified Limits, and Enforcement Analytical Method.	880.1100 880.1400 830.1700 830.1750 830.1800	The information contained in this MRID characterizes the genetic construct used to create OX5034 <i>Ae. aegypti</i> , the active and inert ingredients, the female-specific lethality of the active ingredient, as well as other relevant characteristics of the end-use product. For example, information was provided on the enforcement analytical methods and a discussion of the likelihood for resistance development. The MRID was overall acceptable to characterize the OX5034 <i>Ae. aegypti</i> end-use product. Classification: Acceptable.	50889401 51115102
Quantitative Western Blot Analysis of Expressed Proteins tTAV-OX5034 and DsRed2-OX5034 in OX5034 <i>Aedes aegypti</i> male adults, pupae and larvae.	N/A	The data presented in this study allowed for a conservative estimation of the DsRed2-OX5034 protein abundance in homozygous OX5034 males at all life stages. The data showed that a tTAV protein variant is present in older homozygous OX5034 males but were not adequate to determine total tTAV-OX5034 protein abundance. The SUPPLEMENTAL classification is a result of several methodological deficiencies identified in the immunoblot assays. Classification: Supplemental.	50889419 51094401 51115101
Evaluation of Insecticide Resistance in OX5034	N/A	The data and information presented in the four MRIDs were acceptable to address the insecticide susceptibility of the OX5034 <i>Ae. aegypti</i> strain. OX5034 was susceptible to the pesticide active ingredients Temephos (larvicide), Permethrin, Deltamethrin, and Malathion (three adulticides), and the strain does not carry pyrethroid resistance-associated <i>kdr</i> mutations. It is expected that these four insecticides are effective for controlling OX5034 <i>Ae. aegypti</i> in the field. While the strain showed some resistance to Propoxur, this chemical is not approved for uses on mosquitoes in the U.S. and thus any resistance associated with Propoxur will not affect current mosquito control practices. Classification: Acceptable.	50698717 50698718 50889418 50973405
Arbovirus testing	N/A	TBD	50698723 50889425
The self-limiting phenotype, penetrance, longevity and egg clutch size of <i>Aedes aegypti</i> , OX5034	N/A	Hemizygous and homozygous OX5034 mosquitoes were evaluated for longevity and compared against LWT mosquitoes. Similar longevity between hemizygous OX5034 males and LWT males but reduced longevity in homozygous OX5034 males was found. For egg clutch analysis, crosses were performed between homozygous OX5034 and LWT mosquitoes. Egg clutches are smaller from an OX5034 mating compared to LWT, indicating a potential fitness cost of the OX5034 rDNA. Classification: Acceptable.	50889417

B. Human Health Assessment

1. Toxicological profile

EPA has reviewed the available scientific data and other relevant information in support of this action and considered its validity, completeness and reliability and the relationship of this information to human health risk.

The human health studies submitted for OX5034 are summarized in Table 4 below.

Table 4. Summary of OX5034 Human Health Data.

Study type/ Title	OPPTS Guideline No.	Results Summary and Classification	MRID #
Acute oral toxicity	870.1100	This assessment was based on the information provided by the applicant as part of the scientific rationales, information on the product provided in other parts of the application, and information from the scientific literature. The information provided on the hazard assessment of tTAV-OX5034 and DsRed2-OX5034 is, on its own, inadequate to support the waiver requests. However, exposure to OX5034, tTAV-OX5034, DsRed2-OX5034 and the genetic material encoding them through the dermal, oral, pulmonary, and ocular routes of exposure is expected to be negligible. Therefore, overall the waiver requests for the acute oral toxicity, acute inhalation toxicity, acute dermal toxicity, primary eye irritation, and primary dermal irritation are acceptable. The statement on the occurrence of hypersensitivity incidents is acceptable. Classification: Acceptable.	50889402
Acute inhalation toxicity	870.1300		50889403
Acute eye irritation	870.2400		50889404
Primary dermal irritation	870.2500		50889405
Acute dermal toxicity	870.1200		51086001
Hypersensitivity	N/A		50889406
The self-limiting phenotype, penetrance, longevity and egg clutch size of <i>Aedes aegypti</i> , OX5034; Evaluation of field penetrance of OX5034 in open release field trials in Indaiatuba, São Paulo State, Brazil; Supplemental information in support of the study.	N/A	For penetrance, both laboratory and field studies were performed. Laboratory crosses of OX5034 mosquitoes and wild-type mosquitoes found that no OX5034 females reached the adult stage, confirming 100% penetrance of the OX5034 phenotype. An additional study using field collected eggs from OX5034 releases in Brazil also found complete penetrance of the OX5034 phenotype. The field study indicates that the OX5034 phenotype still results in female lethality even when the OX5034 rDNA is placed in a different genetic background. Finally, the study confirmed the ability of fluorescent screening to determine presence/absence of the OX5034 rDNA by performing PCR-based genotyping. Classification: Acceptable.	50889417 50889423 50889428
Dose response of hemizygous <i>Aedes aegypti</i> OX5034 to tetracyclines and effects of environmental	N/A	The dose-response of OX5034 mosquitoes to a range of tetracycline analogues required to rescue female OX5034 mosquitoes was evaluated. A literature review of tetracycline levels resulting from industrial or household tetracycline usage found that the environmental concentrations of tetracycline analogues appear to be below the levels required to fully rescue	50889415

exposure to tetracyclines		adult females capable of maintaining flight. A local survey of environmental concentrations in the EUP treatment areas and investigation into tetracycline degradates would improve the study. Classification: Supplemental.	
Bioinformatics analysis for risks of allergenicity and toxicity of tTAV-OX5034 and DsRed2-OX5034 (<i>in silico</i> and literature review)	N/A	The study provided bioinformatics analysis on the allergic and toxic potential of the tTAV-OX5034 and DsRed2-OX5034 proteins that were based on protein homology to known allergens and toxins and provided a literature review of the organisms from which these proteins (and their individual sequence components) were derived. The data presented in this study were determined to be supplemental to the overall evaluation of toxicity and allergenicity of the two proteins. No determination of the allergic or toxic potential for tTAV-OX5034 and DsRed2-OX5034 has been made at this time. Classification: Supplemental.	50889420
Protein digestibility and environmental degradation of OX5034 tTAV-OX5034 and DsRed2-OX5034 proteins by proteases, and likelihood of these proteins crossing a cell membrane.	N/A	<i>In silico</i> analyses predict that both the cleaved and uncleaved version of the tTAV-OX5034 variant as well as DsRed2-OX5034 are susceptible to degradation by several proteases present in the human gastric system and the environmental protease proteinase K. These studies were classified as acceptable. The <i>in vitro</i> assay results confirmed some, but not all of the results obtained from the <i>in silico</i> analyses. Due to uncertainties in some of the <i>in vitro</i> data, the study was overall classified as supplemental. In a separate bioinformatics-based assay, it was shown that, based on the overall charge density of the tTAV-OX5034 (both cleaved and uncleaved variants of the F2 transcript) and DsRed2-OX5034, these proteins are unlikely to cross cell membranes. The analysis was classified as acceptable. Classification: Supplemental.	50889421

2. Mammalian toxicity and allergenicity assessment

a. Toxicity assessment

Toxicity of the OX5034-expressed proteins was evaluated through protein sequence comparison with known toxins that are deposited in the NCBI databases using the BLASTp program coupled with the limiting keywords “toxin” and “toxic.” Unlike for the allergenicity assessment, no curated databases or unified guidelines for the *in silico* assessment of novel proteinaceous toxins have been established for use by regulators and the regulated community. The current study relied on protein sequence identity with known toxins deposited in the NCBI database and utilized the Codex guidelines to identify significant matches. It is expected that this approach is likely to have uncovered relevant results because the search was conducted as a global sequence alignment, used a conservative identity threshold, and evaluated the literature associated with those proteins that shared greater than 35% sequence identity. At this level of identity, proteins are generally expected to have similar tertiary structures [ADDIN EN.CITE ADDIN EN.CITE.DATA], which may reflect similar biological activities. This analysis was coupled with subsequent review of the literature associated with the identified NCBI entry. This latter step is important as sequences identified through BLASTp are obtained from several sources, including translation from annotated coding regions in GenBank, RefSeq, and third-party annotation (TPA), as well as records from

SwissProt, Protein Information Resource (PIR; website: <https://pir.georgetown.edu/>), Protein Research Foundation (PRF), and Protein Data Bank (PDB) and therefore not every significant match with a protein deposited in NCBI may also be biologically relevant. Separately, the company also conducted a literature search to evaluate the toxic potential of the source organisms for the individual components of the tTAV-OX5034 and DsRed2-OX5034 proteins.

i. tTAV-OX5034

The tTAV-OX5034 protein is a chimeric fusion of the minimally altered *Aeadsx* splicing module from *Ae. aegypti*, ubiquitin (UBQ) from *D. melanogaster*, linker sequences, and tTAV. The latter is itself a fusion of the tetracycline repressor (TetR) from *E. coli* and the viral tegument protein 16 (VP16) from the Herpes simplex virus-1 (HSV-1; Unit II.A.1.). Using the search criteria outlined above, tTAV-OX5034 showed significant homology to other tetracycline-controlled transactivator (tTA) proteins in the NCBI databases but not to known toxins. A literature review using “tTAV” as a key word revealed that the protein and its components are generally well tolerated when expressed *in vivo*. For example, the TetR domain has been successfully expressed in mice, demonstrating a certain tolerance to this part of the tTAV-OX5034 protein [ADDIN EN.CITE

<EndNote><Cite><Author>Schonig</Author><Year>2013</Year><RecNum>31</RecNum><DisplayText>(Schonig et al. 2013)</DisplayText><record><rec-number>31</rec-number><foreign-keys><key app="EN" db-id="212pdevxize0spe5fsvxsf1fd5zwa2ex2s5" timestamp="1586388674">31</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Schonig, K.</author><author>Freundlieb, S.</author><author>Gossen, M.</author></authors></contributors><auth-address>Heidelberg Univ, Med Fac Mannheim, Cent Inst Mental Hlth, Mannheim, GermanyTET Syst GmbH, Heidelberg, GermanyBerlin Brandenburg Ctr Regenerat Therapies BCRT, D-13353 Berlin, GermanyMax Delbrück Ctr Mol Med, Berlin, Germany</auth-address><titles><title>Tet-Transgenic Rodents: a comprehensive, up-to date database</title><secondary-title>Transgenic Research</secondary-title><alt-title>Transgenic Res</alt-title></titles><periodical><full-title>Transgenic Research</full-title><abbr-1>Transgenic Res</abbr-1></periodical><alt-periodical><full-title>Transgenic Research</full-title><abbr-1>Transgenic Res</abbr-1></alt-periodical><pages>251-254</pages><volume>22</volume><number>2</number><keywords><keyword>tet system</keyword><keyword>transactivator lines</keyword><keyword>responder lines</keyword><keyword>database</keyword><keyword>gene-expression</keyword><keyword>mammalian-cells</keyword></keywords><dates><year>2013</year><pub-dates><date>Apr</date></pub-dates></dates><isbn>0962-8819</isbn><accession-num>WOS:000316065900001</accession-num><urls><related-urls><url><Go to ISI>;//WOS:000316065900001</url></related-urls></urls><electronic-resource-num>10.1007/s11248-012-9660-9</electronic-resource-num><language>English</language></record></Cite></EndNote>]. Furthermore, rabbits survived immunization with the VP16 antigen to produce the polyclonal antibody (AbCam; MRID 50889419), which demonstrates a certain level of mammalian tolerance to that part of the tTAV-OX5034 protein via injection. Some adverse effects have been observed in transgenic mice that expressed tTA proteins, which manifested in emphysema-like symptoms in the lungs and neuronal loss [ADDIN EN.CITE ADDIN EN.CITE.DATA]. However, these effects are generally thought to be the result of differential gene expression mediated by the tTA protein and there is no indication from the literature that these effects are due to an inherent toxicity of the protein [ADDIN EN.CITE ADDIN EN.CITE.DATA].

The modified *Aeadsx* protein, which comprises the N-terminus of tTAV-OX5034, is endogenous to *Ae. aegypti* and thus is not expected to be toxic to insects. UBQ was fused in between *Aeadsx* and tTAV to facilitate release of the active tTAV variant from the full-length protein subsequent to translation. While this particular UBQ protein sequence was derived from *D. melanogaster*, UBQ is structurally and

functionally regarded as one of the most highly conserved proteins in Eukaryota and therefore is expected to be well tolerated by these organisms [ADDIN EN.CITE ADDIN EN.CITE.DATA].

Due to the lethal nature of the Tet-OFF gene circuit engineered into the OX5034 strain, it is difficult to distinguish between adverse effects that are the result of transcriptional squelching and adverse effects that may be the result of tTAV-OX5034 toxicity. However, it remains relevant to note that male adult OX5034 mosquitoes express the tTAV-OX5034 mRNA and can complete their life cycle (Units II.A.3. and 4.b.).

In summary, the information presented in this study, supplemented with information from other parts of the application and the published scientific literature, support the finding that the individual components of the tTAV-OX5034 protein are well tolerated in several eukaryotic organisms and that there is no indication that the two variants of the tTAV-OX5034 protein, uncleaved and cleaved, share significant protein homology to known toxins. Lastly, there is no indication in the literature to suggest that the source organisms of the various proteins that comprise the tTAV-OX5034 protein have toxic characteristics.

ii. DsRed2-OX5034

Using the search criteria outlined above, the DsRed2-OX5034 protein showed no significant homology to known toxins but shared significant similarity with other fluorescent proteins. Fluorescent proteins have many applications in molecular cell biology, including as gene expression markers, protein tags, and for investigating protein-protein interactions *in vivo*. To that end, in addition to OX5034 *Ae. aegypti*, other transgenic organisms stably expressing DsRed2 and related protein derivatives have been created including other insects [ADDIN EN.CITE ADDIN EN.CITE.DATA], fungi [ADDIN EN.CITE
<EndNote><Cite><Author>Nahalkova</Author><Year>2003</Year><RecNum>23</RecNum><DisplayText>(Nahalkova and Fatehi 2003)</DisplayText><record><rec-number>23</rec-number><foreign-keys><key app="EN" db-id="2t2pdevxize0spe5fsvxsf1fd5zwa2ex2s5" timestamp="1586388365">23</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Nahalkova, J.</author><author>Fatehi, J.</author></authors></contributors><auth-address>Department of Molecular Evolution, Uppsala University, Norbyvagen 18C, S-75236 Uppsala, Sweden. jarmila.nahalkova@ebc.uu.se</auth-address><titles><title>Red fluorescent protein (DsRed2) as a novel reporter in *Fusarium oxysporum* f. sp. *lycopersici*</title><secondary-title>FEMS Microbiol Lett</secondary-title></titles><periodical><full-title>FEMS Microbiol Lett</full-title></periodical><pages>305-9</pages><volume>225</volume><number>2</number><edition>2003/09/03</edition><keywords><keyword>Aspergillus nidulans/enzymology</keyword><keyword>Cloning, Molecular</keyword><keyword>Fluorescence</keyword><keyword>Fusarium/*genetics/growth & development/*metabolism/pathogenicity</keyword><keyword>Gene Expression Regulation, Fungal</keyword><keyword>Genes</keyword><keyword>*Genes, Reporter</keyword><keyword>Glycerol-3-Phosphate Dehydrogenase (NAD+)</keyword><keyword>Glycerolphosphate Dehydrogenase/genetics</keyword><keyword>Luminescent Proteins/*genetics/*metabolism</keyword><keyword>Lycopersicon esculentum/microbiology</keyword><keyword>Microscopy, Fluorescence</keyword><keyword>Promoter Regions, Genetic</keyword><keyword>Transformation, Genetic</keyword></keywords><dates><year>2003</year><pub-dates><date>Aug 29</date></pub-dates></dates><isbn>0378-1097 (Print)0378-1097 (Linking)</isbn><accession-num>12951257</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/12951257</url></related-urls></urls><electronic-resource-num>10.1016/S0378-1097(03)00534-2</electronic-resource-num></record></Cite></EndNote>], plants (Nishizawa [ADDIN EN.CITE
<EndNote><Cite><Author>Nishizawa</Author><Year>2006</Year><RecNum>24</RecNum><Display

yText>(Nishizawa et al. 2006)</DisplayText><record><rec-number>24</rec-number><foreign-keys><key app="EN" db-id="2t2pdevxize0spe5fsvxsf1fd5zwa2ex2s5" timestamp="1586388486">24</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Nishizawa, K.</author><author>Kita, Y.</author><author>Kitayama, M.</author></authors><auth-address>Natl Agr Res Ctr Hokkaido Reg, Sapporo, Hokkaido 0628555, JapanEhime Womens Coll, Uwajima, Ehime 7980025, Japan</auth-address><titles><title>A red fluorescent protein, DsRed2, as a visual reporter for transient expression and stable transformation in soybean</title><secondary-title>Plant Cell Reports</secondary-title><alt-title>Plant Cell Rep</alt-title></titles><periodical><full-title>Plant Cell Reports</full-title><abbr-1>Plant Cell Rep</abbr-1></periodical><alt-periodical><full-title>Plant Cell Reports</full-title><abbr-1>Plant Cell Rep</abbr-1></alt-periodical><pages>1355-1361</pages><volume>25</volume><number>12</number><keywords><keyword>bombardment</keyword><keyword>dsred2</keyword><keyword>fluorescent protein</keyword><keyword>nondestructive</keyword><keyword>transgenic soybean</keyword><keyword>living plants</keyword><keyword>discosoma sp</keyword><keyword>green</keyword><keyword>transgenes</keyword></keywords><dates><year>2006</year><pub-dates><date>Dec</date></pub-dates></dates><isbn>0721-7714</isbn><accession-num>WOS:000242150200012</accession-num><urls><related-urls><url><Go to ISI>;//WOS:000242150200012</url></related-urls></urls><electronic-resource-num>10.1007/s00299-006-0210-x</electronic-resource-num><language>English</language></record></Cite></EndNote>], mice [ADDIN EN.CITE <EndNote><Cite><Author>Ryu</Author><Year>2013</Year><RecNum>29</RecNum><DisplayText>(Ryu et al. 2013)</DisplayText><record><rec-number>29</rec-number><foreign-keys><key app="EN" db-id="2t2pdevxize0spe5fsvxsf1fd5zwa2ex2s5" timestamp="1586388674">29</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Ryu, J. Y.</author><author>Siswanto, A.</author><author>Harimoto, K.</author><author>Tagawa, Y.</author></authors><auth-address>Tokyo Inst Technol, Dept Biomol Engn, Grad Sch Biosci & Biotechnol, Midori Ku, Yokohama, Kanagawa 2268503, Japan</auth-address><titles><title>Chimeric analysis of EGFP and DsRed2 transgenic mice demonstrates polyclonal maintenance of pancreatic acini</title><secondary-title>Transgenic Research</secondary-title><alt-title>Transgenic Res</alt-title></titles><periodical><full-title>Transgenic Research</full-title><abbr-1>Transgenic Res</abbr-1></periodical><alt-periodical><full-title>Transgenic Research</full-title><abbr-1>Transgenic Res</abbr-1></alt-periodical><pages>549-556</pages><volume>22</volume><number>3</number><keywords><keyword>pancreatic maintenance</keyword><keyword>pancreatic acinus</keyword><keyword>chimera</keyword><keyword>egfp</keyword><keyword>dsred2</keyword><keyword>developmental biology</keyword><keyword>progenitor cells</keyword><keyword>mouse chimeras</keyword><keyword>beta-cells</keyword><keyword>expression</keyword><keyword>islets</keyword></keywords><dates><year>2013</year><pub-dates><date>Jun</date></pub-dates></dates><isbn>0962-8819</isbn><accession-num>WOS:000319008400007</accession-num><urls><related-urls><url><Go to ISI>;//WOS:000319008400007</url></related-urls></urls><electronic-resource-num>10.1007/s11248-012-9661-8</electronic-resource-num><language>English</language></record></Cite></EndNote>], and rats [ADDIN EN.CITE <EndNote><Cite><Author>Sato</Author><Year>2003</Year><RecNum>30</RecNum><DisplayText>(Sato et al. 2003)</DisplayText><record><rec-number>30</rec-number><foreign-keys><key app="EN" db-id="2t2pdevxize0spe5fsvxsf1fd5zwa2ex2s5" timestamp="1586388674">30</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Sato, Y.</author><author>Igarashi, Y.</author><author>Hakamata, Y.</author><author>Murakami, T.</author><author>Kaneko,

T. /author><author>Takahashi, M. /author><author>Seo, N. /author><author>Kobayashi, E. /author></authors></contributors><auth-address>Jichi Med Sch, Ctr Mol Med, Div Organ Replacement Res, Kawachi, Tochigi, JapanJichi Med Sch, Dept Anesthesiol, Kawachi, Tochigi, Japan</auth-address><titles><title>Establishment of Alb-DsRed2 transgenic rat for liver regeneration research</title><secondary-title>Biochemical and Biophysical Research Communications</secondary-title><alt-title>Biochem Bioph Res Co</alt-title></titles><periodical><full-title>Biochemical and Biophysical Research Communications</full-title><abbr-1>Biochem Bioph Res Co</abbr-1></periodical><alt-periodical><full-title>Biochemical and Biophysical Research Communications</full-title><abbr-1>Biochem Bioph Res Co</abbr-1></alt-periodical><pages>478-481</pages><volume>311</volume><number>2</number><keywords><keyword>red fluorescent protein</keyword><keyword>bone-marrow</keyword><keyword>stem-cells</keyword><keyword>hepatocytes</keyword><keyword>mice</keyword><keyword>fusion</keyword><keyword>expression</keyword><keyword>molecule</keyword><keyword>tool</keyword></keywords><dates><year>2003</year><pub-dates><date>Nov 14</date></pub-dates></dates><isbn>0006-291x</isbn><accession-num>WOS:000186584100035</accession-num><urls><related-urls><url><Go to ISI>;//WOS:000186584100035</url></related-urls></urls><electronic-resource-num>10.1016/j.bbrc.2003.09.230</electronic-resource-num><language>English</language></record></Cite></EndNote>]. The successful expression of these related proteins speaks to a certain level of tolerance by eukaryotic organisms, including mammals. Rabbits in particular tolerate immunization with the DsRed-Express antigen for the production of polyclonal antibody, which indicates mammalian tolerance to this DsRed protein variant through injection (TaKaRa – Clontech; MRID 50889419).

However, cytotoxic effects have also been observed in association with the heterologous expression of fluorescent proteins such as those discussed above, including variants of DsRed2. Adverse effects manifested in the failure of obtaining stably expressing mammalian transformants and reduced growth of transformed mammalian cell lines [[ADDIN EN.CITE <EndNote><Cite><Author>Hadjantonakis</Author><Year>2002</Year><RecNum>17</RecNum><DisplayText>(Hadjantonakis et al. 2002)</DisplayText><record><rec-number>17</rec-number><foreign-keys><key app="EN" db-id="2t2pdevxize0spe5fsvxsf1fd5zwa2ex2s5" timestamp="1586388224">17</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Hadjantonakis, A. K.</author><author>Macmaster, S.</author><author>Nagy, A.</author></authors></contributors><auth-address>Samuel Lunenfeld Research Institute, Mount Sinai Hospital, Toronto, Canada. akh39@columbia.edu</auth-address><titles><title>Embryonic stem cells and mice expressing different GFP variants for multiple non-invasive reporter usage within a single animal</title><secondary-title>BMC Biotechnol</secondary-title></titles><periodical><full-title>BMC Biotechnol</full-title></periodical><pages>11</pages><volume>2</volume><edition>2002/06/25</edition><keywords><keyword>Animals</keyword><keyword>Cells, Cultured</keyword><keyword>Chimera</keyword><keyword>Electroporation</keyword><keyword>Feasibility Studies</keyword><keyword>Gene Expression Regulation/*physiology</keyword><keyword>Gene Transfer Techniques</keyword><keyword>*Genes, Reporter</keyword><keyword>Green Fluorescent Proteins</keyword><keyword>Luminescent Proteins/*biosynthesis/genetics</keyword><keyword>Mice</keyword><keyword>Mice, Transgenic/*genetics</keyword><keyword>Organ Specificity</keyword><keyword>Stem Cells/cytology/*metabolism</keyword></keywords><dates><year>2002</year><pub-dates><date>Jun 11</date></pub-dates></dates><isbn>1472-6750 (Electronic)1472-6750 (Linking)</isbn><accession-num>12079497</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/12079497</url></related-urls></urls><custom2>PMC116589</custom2><electronic-resource-num>10.1186/1472-6750-2-11</electronic-resource-num></record></Cite></EndNote>] (DsRed); [ADDIN EN.CITE

<EndNote><Cite><Author>Koelsch</Author><Year>2013</Year><RecNum>21</RecNum><DisplayText>(Koelsch et al. 2013)</DisplayText><record><rec-number>21</rec-number><foreign-keys><key app="EN" db-id="2t2pdevxize0spe5fsvxsfflfd5zwa2ex2s5" timestamp="1586388224">21</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Koelsch, K. A.</author><author>Wang, Y.</author><author>Maier-Moore, J. S.</author><author>Sawalha, A. H.</author><author>Wren, J. D.</author></authors></contributors><auth-address>Oklahoma Medical Research Foundation, Arthritis and Clinical Immunology Program, Oklahoma City, Oklahoma, USA. Kristi-Koelsch@omrf.org</auth-address><titles><title>GFP affects human T cell activation and cytokine production following in vitro stimulation</title><secondary-title>PLoS One</secondary-title></titles><periodical><full-title>PLoS One</full-title></periodical><pages>e50068</pages><volume>8</volume><number>4</number><edition>2013/04/12</edition><keywords><keyword>Biomarkers/metabolism</keyword><keyword>Cytokines/*biosynthesis</keyword><keyword>Gene Expression Regulation</keyword><keyword>Green Fluorescent Proteins/*metabolism</keyword><keyword>HEK293 Cells</keyword><keyword>HeLa Cells</keyword><keyword>Humans</keyword><keyword>Interleukin-2/metabolism</keyword><keyword>Interleukin-2 Receptor alpha Subunit/genetics</keyword><keyword>*Lymphocyte Activation</keyword><keyword>NF-kappa B/antagonists & inhibitors</keyword><keyword>RNA, Messenger/genetics/metabolism</keyword><keyword>T-Lymphocytes/*immunology/*metabolism</keyword></keywords><dates><year>2013</year></dates><isbn>1932-6203 (Electronic)1932-6203 (Linking)</isbn><accession-num>23577054</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/23577054</url></related-urls></urls><custom2>PMC3618152</custom2><electronic-resource-num>10.1371/journal.pone.0050068</electronic-resource-num></record></Cite></EndNote>] (GFP); [ADDIN EN.CITE

<EndNote><Cite><Author>Zakrzewska</Author><Year>2014</Year><RecNum>37</RecNum><DisplayText>(Zakrzewska et al. 2014)</DisplayText><record><rec-number>37</rec-number><foreign-keys><key app="EN" db-id="2t2pdevxize0spe5fsvxsfflfd5zwa2ex2s5" timestamp="1586388735">37</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Zakrzewska, K. E.</author><author>Samluk, A.</author><author>Pluta, K. D.</author><author>Pijanowska, D. G.</author></authors></contributors><auth-address>PAS, Nalecz Inst Biocybernet & Biomed Engn, Dept Hybrid Microbiosyst Engn, Warsaw, Poland</auth-address><titles><title>Evaluation of the effects of antibiotics on cytotoxicity of EGFP and DsRed2 fluorescent proteins used for stable cell labeling</title><secondary-title>Acta Biochimica Polonica</secondary-title><alt-title>Acta Biochim Pol</alt-title></titles><periodical><full-title>Acta Biochimica Polonica</full-title><abbr-1>Acta Biochim Pol</abbr-1></periodical><alt-periodical><full-title>Acta Biochimica Polonica</full-title><abbr-1>Acta Biochim Pol</abbr-1></alt-periodical><pages>809-813</pages><volume>61</volume><number>4</number><keywords><keyword>stable fluorescent labeling</keyword><keyword>whole-cell labeling</keyword><keyword>fluorescent protein cytotoxicity</keyword><keyword>expression</keyword><keyword>runx2</keyword></keywords><dates><year>2014</year></dates><isbn>0001-527x</isbn><accession-num>WOS:000347435900028</accession-num><urls><related-urls><url><Go to ISI>://WOS:000347435900028</url></related-urls></urls><language>English</language></record></Cite></EndNote>] (DsRed2)]. Only a few studies could be found in the literature that explored the potential cytotoxic mechanisms for DsRed variants [[ADDIN EN.CITE

<EndNote><Cite><Author>Zhou</Author><Year>2011</Year><RecNum>38</RecNum><DisplayText>(Zhou et al. 2011)</DisplayText><record><rec-number>38</rec-number><foreign-keys><key app="EN" db-id="2t2pdevxize0spe5fsvxsfflfd5zwa2ex2s5"

timestamp="1586388772">38</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Zhou, J.</author><author>Lin, J.</author><author>Zhou, C.</author><author>Deng, X.</author><author>Xia, B.</author></authors></contributors><auth-address>Key Laboratory for Biomechanics and Mechanobiology of Ministry of Education, School of Biological Science and Biomedical Engineering, Beihang University, China.</auth-address><titles><title>Cytotoxicity of red fluorescent protein DsRed is associated with the suppression of Bcl-xL translation</title><secondary-title>FEBS Lett</secondary-title></titles><periodical><full-title>FEBS Lett</full-title></periodical><pages>821-7</pages><volume>585</volume><number>5</number><edition>2011/02/16</edition><keywords><keyword>Cell Death</keyword><keyword>Down-Regulation</keyword><keyword>Flow Cytometry</keyword><keyword>Green Fluorescent Proteins/metabolism</keyword><keyword>HeLa Cells</keyword><keyword>Humans</keyword><keyword>Luminescent Proteins/*metabolism</keyword><keyword>Microscopy, Fluorescence</keyword><keyword>*Protein Biosynthesis</keyword><keyword>Protein Isoforms/metabolism</keyword><keyword>bcl-X Protein/*biosynthesis</keyword></keywords><dates><year>2011</year><pub-dates><date>Mar 9</date></pub-dates></dates><isbn>1873-3468 (Electronic)0014-5793 (Linking)</isbn><accession-num>21320495</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/21320495</url></related-urls></urls><electronic-resource-num>10.1016/j.febslet.2011.02.013</electronic-resource-num></record></Cite></EndNote>] (DsRed and DsRed-Express2)] and many of those effects are attributed to protein tetramerization and aggregation resulting from the constitutive expression of these proteins *in vivo* [ADDIN EN.CITE ADDIN EN.CITE.DATA].

The DsRed2 protein variant served as the blueprint for the development of DsRed2-OX5034. DsRed2 itself was originally created in search of a DsRed1 variant with reduced aggregation properties and low cytotoxicity. Three N-terminal amino acid (R2A, K5E, and K9T) substitutions in DsRed1 increased protein solubility and generally reduced cytotoxicity [ADDIN EN.CITE <EndNote><Cite><Author>Yanushevich</Author><Year>2002</Year><RecNum>36</RecNum><DisplayText>(Yanushevich et al. 2002)</DisplayText><record><rec-number>36</rec-number><foreign-keys><key app="EN" db-id="2t2pdevxize0spe5fsvxsf1fd5zwa2ex2s5" timestamp="1586388715">36</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Yanushevich, Y. G.</author><author>Staroverov, D. B.</author><author>Savitsky, A. P.</author><author>Fradkov, A. F.</author><author>Gurskaya, N. G.</author><author>Bulina, M. E.</author><author>Lukyanov, K. A.</author><author>Lukyanov, S. A.</author></authors></contributors><auth-address>Shemyakin and Ovchinnikov Institute of Bioorganic Chemistry RAS, Moscow, Russia.</auth-address><titles><title>A strategy for the generation of non-aggregating mutants of Anthozoa fluorescent proteins</title><secondary-title>FEBS Lett</secondary-title></titles><periodical><full-title>FEBS Lett</full-title></periodical><pages>11-4</pages><volume>511</volume><number>1-3</number><edition>2002/02/01</edition><keywords><keyword>Amino Acid Substitution/genetics</keyword><keyword>Animals</keyword><keyword>Cloning, Molecular</keyword><keyword>*Cnidaria/chemistry/genetics</keyword><keyword>Color</keyword><keyword>Electrophoresis, Polyacrylamide Gel</keyword><keyword>Fluorescence</keyword><keyword>Luminescent Proteins/chemistry/*genetics/*metabolism</keyword><keyword>Molecular Weight</keyword><keyword>Mutagenesis, Site-Directed/genetics</keyword><keyword>Mutation/*genetics</keyword><keyword>Protein Binding</keyword><keyword>Protein Structure, Quaternary</keyword></keywords><dates><year>2002</year><pub-dates><date>Jan 30</date></pub-dates></dates><isbn>0014-5793 (Print)0014-5793 (Linking)</isbn><accession-num>11821040</accession-num><urls><related-

<https://www.ncbi.nlm.nih.gov/pubmed/11821040>

DsRed2-OX5034 is virtually identical to this DsRed2 variant, but in addition contains a bipartite NLS and linker sequences at its N- and C-terminus (resulting in a protein that is 15% larger). The N-terminal NLS was originally identified in the SV40 large T-antigen in humans, and as such is unlikely to cause mammalian toxicity concerns by itself [ADDIN EN.CITE

(Kalderon et al. 1984)

Sequence requirements for nuclear location of simian virus 40 large-T antigen

Nature

Nature

33-8

311

5981

1984/09/06

Animals

Antigens, Polyomavirus

Transforming

Base Sequence

Cell

Line

Cell Nucleus/*analysis

Cell Transformation,

Viral

*DNA Replication

DNA Restriction

Enzymes

Mutation

Nucleic Acid

Hybridization

Plasmids

Rats

Simian virus 40/*genetics

Viral

Proteins/*genetics

1984

Sep 6-11

0028-0836 (Print)0028-0836 (Linking)

6088992

<https://www.ncbi.nlm.nih.gov/pubmed/6088992>

The C-terminal NLS is very similar in sequence, but it is unclear from the study whether it is a native or a synthetic NLS. Given that the composition of the N-terminus appears to be an important determinant for the tendency of DsRed2 to aggregate when expressed *in vivo*, it is not possible to anticipate the behavior of DsRed2-OX5034 and to what extent this may affect the cytotoxic characteristics of the protein. It is relevant to note that these adverse effects were observed in the context of *in vivo* expression (both transient and constitutive), which represents a uniquely high exposure scenario for these transgenic organisms and cell lines, especially when the protein is expressed constitutively. *In vivo* expression of proteins can also disrupt normal cellular function, which in turn may have contributed to the observed adverse effects.

In summary, DsRed2-OX5034 does not share significant homology to known toxins. Information from the literature suggests that, while some DsRed variants are cytotoxic when expressed *in vivo*, there is no evidence to suggest that they are inherently toxic. This is supported by their broad use as fluorescence markers in several organisms, including mammals. Further, polyclonal antibodies for a DsRed variant were successfully produced in rabbits, a process that usually requires several rounds of injections, either subcutaneous, intradermal, intramuscular, intraperitoneal, or intravenous route[ADDIN EN.CITE

(Leenaars and Hendriksen 2005)

Critical steps in the production of polyclonal and monoclonal

antibodies: evaluation and recommendations</title><secondary-title>ILAR J</secondary-title></titles><periodical><full-title>ILAR J</full-title></periodical><pages>269-79</pages><volume>46</volume><number>3</number><edition>2005/06/15</edition><keywords><keyword>Adjuvants, Immunologic/pharmacology</keyword><keyword>Animal Welfare</keyword><keyword>Animals</keyword><keyword>Antibodies, Monoclonal/*biosynthesis</keyword><keyword>Antibody Formation/*immunology</keyword><keyword>Antigens/administration & dosages</keyword><keyword>Ascites/immunology</keyword><keyword>B-Lymphocytes/*immunology</keyword><keyword>Female</keyword><keyword>Guidelines as Topic</keyword><keyword>Hybridomas/immunology</keyword><keyword>Immunization/*methods</keyword><keyword>Male</keyword></keywords><dates><year>2005</year></dates><isbn>1084-2020 (Print)1084-2020 (Linking)</isbn><accession-num>15953834</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/15953834</url></related-urls></urls><electronic-resource-num>10.1093/ilar.46.3.269</electronic-resource-num></record></Cite></EndNote>]. Lastly, there is no indication in the literature to suggest that *Discosoma sp.*, from which DsRed2-OX5034 was derived, has toxic characteristics.

b. Allergenicity assessment

Bioinformatics analyses of the primary protein sequence of tTAV-OX5034 and DsRed2-OX5034 were performed using three databases, AllergenOnline (Food Allergy Research & Resource Program, University of Nebraska), COMPARE (Comprehensive Protein Allergen Resource, Health and Environmental Sciences Institute (HESI)), and the NCBI Entrez Protein database using “allergen” as a restricting keyword. These bioinformatics analyses commonly help determine the potential for IgE cross-reactivity. AllergenOnline and COMPARE are curated databases for putative and known food and non-food allergens, including mosquito allergens, while the NCBI Entrez Protein database is not restricted to allergenic proteins. In addition, a literature search was also conducted to evaluate the allergic potential of the source organisms for the individual components of the tTAV-OX5034 and DsRed2-OX5034 proteins.

i. tTAV-OX5034

tTAV-OX5034 did not show significant homology with any allergenic proteins. The uncleaved form of the tTAV-OX5034 protein (which is expressed in adult males MRID 50889401) is a chimeric fusion protein of the minimally altered *Aeadsx* splicing module from *Ae. aegypti*, the tetracycline repressor (TetR) from *E. coli*, the viral tegument protein 16 (VP16) from the Herpes simplex virus-1 (HSV-1), ubiquitin (UBQ) from *D. melanogaster*, and linker sequences. A literature review using keywords related to “*E. coli*” and “Herpes” coupled with the keywords “allergen” and “allergy,” respectively, did not uncover any studies that indicate that these source organisms have allergenic characteristics. Only *Ae. aegypti* is a known source of allergens, as female saliva contains several allergenic proteins. Given that tTAV-OX5034 is a chimeric fusion protein comprised of several proteins from various source organisms and contains only part of the endogenous *Aeadsx* protein, it is questionable whether the allergic properties of *Ae. aegypti* are biologically relevant for evaluating the likelihood of tTAV-OX5034 allergenicity.

ii. DsRed2-OX5034

Specific to DsRed2-OX5034, the study failed to identify and address the significant sequence identities between the DsRed2 protein (as expressed in OX513A; EPA File Symbol 93167-EUP-R) and four predicted protein variants of the GFP-like protein Akane from *Scleronephthya gracillima* that had previously been identified as part of the evaluation of EPA File Symbol 93167-EUP-R. The two expert panels curating the AOL and COMPARE databases initially evaluated the Kato *et al.*, 2017 publication and added the GFP-like protein variants to their respective databases (AOL version v18A and COMPARE version February 01, 2018). However, all four sequences were subsequently removed after

both expert panels reevaluated the publication and independently concluded that the data presented in the study did not, in fact, meet the criteria for adoption. Letters from both AOL and COMPARE panels explaining their respective decisions to remove the GFP-like protein Akane were previously provided by Oxitec as part of the application for the OX513A *Ae. aegypti* product, as well as the proposed application of OX5034 *Ae. aegypti* [ADDIN EN.CITE ADDIN EN.CITE.DATA] (MRID 50889426). A discussion of the data published in Kato *et al.*, 2017 remains relevant for the OX5034 application as DsRed2-OX5034 and the four variants of the GFP-like protein share a level of protein sequence identity that would trigger the need for further characterization of allergenicity under Codex (see Figure 1A, Appendix). Evaluation of the information provided by the applicant in MRID 50889426 is ongoing and no determination on the allergenic potential of DsRed2-OX5034 has been made at this time. There is no indication in the literature to suggest that *Discosoma sp.*, from which DsRed2-OX5034 was derived, has allergenic characteristics.

c. Mammalian toxicity and allergenicity conclusion

Mammalian toxicity and allergenicity of transgenic proteins is commonly evaluated in association with the hazard assessment of plant-incorporated protectants (PIPs) engineered into food plants and is based on a weight-of-evidence approach. As further discussed below, this assessment often considers a combination of data obtained from animal testing, several *in vitro* analyses of the protein, and prediction of protein behavior using bioinformatics tools.

The assessment of protein toxicity is commonly comprised of a combination of acute oral toxicity data generated in rats (OCSPG Guidelines 870.1100), supplemented with homology searches of the protein sequence to known proteinaceous toxins. As discussed in this unit, unlike for the allergenicity assessment of proteins, there are currently no internationally recognized guidelines for evaluating the potential toxicity of a protein based on the presence of specific motifs or homology to known toxins. In support of the toxicity assessment of tTAV-OX5034 and DsRed2-OX5034, Oxitec did not provide acute oral toxicity data, but provided bioinformatics and literature analysis on the potential toxic characteristics of the proteins and the source organisms. The latter did not indicate that either protein is inherently toxic. At this time the Agency has not determined whether the presented protein homology and literature-based assessments alone are sufficient to support the hazard assessment of tTAV-OX5034 and DsRed2-OX5034 and thus has not made a final determination on the potential toxicity of the two proteins.

EPA uses the Codex Alimentarius guidelines to evaluate proteins for their allergic potential [ADDIN EN.CITE

<EndNote><Cite><Author>Alimentarius</Author><Year>2003</Year><RecNum>318</RecNum><DisplayText>(Codex Alimentarius 2003)</DisplayText><record><rec-number>318</rec-number><foreign-keys><key app="EN" db-id="2t2pdevxize0spe5fsvxsf1fd5zwa2ex2s5" timestamp="1586892063">318</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Codex Alimentarius,</author></authors></contributors><titles><title>Codex principles and guidelines on foods derived from biotechnology. Codex Alimentarius Commission, Joint FAO/WHO Food Standards Programme, Food and Agriculture Organisation: Rome.</title><secondary-title>Food and Agriculture Organisation</secondary-title></titles><periodical><full-title>Food and Agriculture Organisation</full-title></periodical><dates><year>2003</year></dates><urls></urls></record></Cite></EndNote>]. The Codex guidelines are based on a weight-of-evidence approach, which generally considers homology to known allergens, allergic characteristics of the source organism from which the protein was derived, proteolytic susceptibility of proteins to gastrointestinal proteases, and protein glycosylation. This information commonly informs the hazard assessment of proteins through the oral and inhalation routes of exposure.

While tTAV-OX5034 did not show significant homology to known allergens, the evaluation of the information provided for DsRed2-OX5034 is still ongoing and no determination has been made. No information was provided on the glycosylation of the two proteins. This post-translational modification is thought to be able to affect exposure to the protein in the digestive system. Data on the proteolytic susceptibility is commonly generated through *in vitro* digestibility assays using the protein isolated from the transgenic organism (in the case of plant-incorporated protectants) or heterologous expressed protein that has been demonstrated to be equivalent to that produced by the transgenic organism, e.g., by demonstrating similar biological activity. This information is often supplemented with bioinformatics analysis to predict potential cleavage sites of relevant gastrointestinal proteases within the primary protein sequence. The digestibility data for tTAV-OX5034 and DsRed2-OX5034 was classified as supplemental and can therefore not be fully utilized to support the allergenicity assessment (MRID 50889421; Table 4). Specifically, while *in silico* analyses show that both proteins are predicted to be susceptible to pepsin, trypsin, and chymotrypsin, no *in vitro* data demonstrating pepsin lability of the uncleaved (full-length) tTAV-OX5034 are available. A DsRed2 variant that is in part identical to the DsRed2-OX5034 protein was previously demonstrated to be rapidly digested by pepsin, but no such data was presented for DsRed-OX5034, which is approx. 15% larger.

In addition to the consideration on the common mammalian hazard assessment approach outlined above, the biology of *Ae. aegypti* is an important consideration for evaluating the potential human exposure to OX5034 and associated traits. Specifically, were OX5034 females to be present in the environment they could pose a hazard through a route of exposure that is not commonly considered by Codex and the human health risk assessment.

Human exposure to *Ae. aegypti* is primarily mediated through females who rely on a blood meal from a vertebrate source to support egg production [ADDIN EN.CITE ADDIN EN.CITE.DATA]. For feeding to occur, the proboscis must break the skin barrier (epidermis) to reach the blood vessels in the dermal layer. During the probing phase, female mosquitoes inject a few nanoliters of saliva intradermally [ADDIN EN.CITE

<EndNote><Cite><Author>Hopp</Author><Year>2015</Year><RecNum>6</RecNum><DisplayText>(Hopp and Sinnis 2015)</DisplayText><record><rec-number>6</rec-number><foreign-keys><key app="EN" db-id="2t2pdevxize0spe5fsvxsfflfd5zwa2ex2s5" timestamp="1586386647">6</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Hopp, C. S.</author><author>Sinnis, P.</author></authors></contributors><auth-address>Department of Molecular Microbiology and Immunology, Johns Hopkins School of Public Health, Baltimore, Maryland; Johns Hopkins Malaria Research Institute, Baltimore, Maryland.</auth-address><titles><title>The innate and adaptive response to mosquito saliva and Plasmodium sporozoites in the skin</title><secondary-title>Ann N Y Acad Sci</secondary-title></titles><periodical><full-title>Ann N Y Acad Sci</full-title></periodical><pages>37-43</pages><volume>1342</volume><edition>2015/02/20</edition><keywords><keyword>Adaptive Immunity/*immunology</keyword><keyword>Animals</keyword><keyword>Culicidae/immunology/parasitology</keyword><keyword>Humans</keyword><keyword>Immunity, Innate/*immunology</keyword><keyword>Plasmodium/*immunology</keyword><keyword>Saliva/*immunology/parasitology</keyword><keyword>Skin/*immunology/parasitology</keyword><keyword>Sporozoites/*immunology/parasitology</keyword><keyword>dermal immune system</keyword><keyword>human adaptive immunity</keyword><keyword>human innate immunity</keyword><keyword>malaria</keyword><keyword>mosquito saliva</keyword><keyword>rodent malaria model</keyword><keyword>sporozoite</keyword></keywords><dates><year>2015</year><pub-dates><date>Apr</date></pub-dates></dates><isbn>1749-6632 (Electronic)0077-8923 (Linking)</isbn><accession-num>25694058</accession-num><urls><related-urls><url>https://www.ncbi.nlm.nih.gov/pubmed/25694058</url></related-

urls></urls><custom2>PMC4405444</custom2><electronic-resource-num>10.1111/nyas.12661</electronic-resource-num></record></Cite></EndNote>]. Female saliva contains anti-hemostatic, anti-inflammatory, and immunosuppressive factors that counteract physiological responses at the bite site and facilitate feeding [ADDIN EN.CITE ADDIN EN.CITE.DATA]. As such, the route of exposure to proteins that are secreted into the saliva of biting female mosquitoes is more accurately described as intradermal. Given the differences in the proteolytic environment between the human gastric system and the dermis, the question arises to what extent the same hazard assessment approach, and Codex guidelines, are applicable.

Proteins that are demonstrated to be susceptible to proteolytic degradation in the human digestive system are thought to have a lower likelihood to elicit adverse effects due to reduced exposure. Some proteins injected by mosquitoes have been detected for up to 18 hours in the skin of mice bitten by *Anopheles gambiae* [ADDIN EN.CITE ADDIN EN.CITE.DATA] and thus, tTAV-OX5034 and DsRed2-OX5034, if injected, may have the potential to elicit prolonged intradermal exposure. Relatedly, the toxic characteristics of a protein may be different when injected into the skin, e.g., snake venom, versus (epi)-dermal exposure, especially in the absence of adjuvants. Mosquito bites furthermore create local inflammatory responses resulting from a combination of the puncturing of the dermis and blood vessels and the presence of naturally occurring allergenic proteins in the mosquito saliva, which may alter the dermal response to a substance at the affected location. Thus, intradermal exposure to a substance is arguably different from dermal exposure. To what extent they are different and how, if at all, this difference may affect the hazard assessment of proteins that pose an intradermal exposure risk remains to be evaluated.

At the time the review was completed, no determination on the toxic and allergic potential of the tTAV-OX5034 and DsRed2-OX5034 proteins was made. Further, the Agency had not determined whether, and if so which, additional data would be needed to support the hazard evaluation for proteins that may pose intradermal exposure, such as tTAV-OX5034 and DsRed2-OX5034. The risk assessment process for pesticide evaluation is characterized by evaluating the hazard and exposure to a particular pesticide product using the basic equation: Risk = Hazard x Exposure. The potential for exposure and the overall risk from OX5034 *Ae. aegypti* is discussed in Unit II.B.3.b.

3. Human exposure and human health risk characterization

a. Penetrance of the female-lethal trait

Laboratory and field studies confirming 100% penetrance in the absence of tetracycline

In the context of this risk assessment, penetrance refers to the proportion of individuals of a given genotype that show the phenotype typical of that genotype. In the case of penetrance of the self-limiting trait of OX5034 strain, this refers to the proportion of female insects that die before reaching adulthood. To confirm that the OX5034 self-limiting trait indeed results in 100% female lethality, laboratory crosses were performed (Table 5). Crosses were reared both with the dietary antidote (a tetracycline analogue), which rescues OX5034 females, and without the dietary antidote. Rearing conditions without the dietary antidote are considered field-like conditions.

Laboratory crosses of OX5034 mosquitoes and LWT mosquitoes found that no OX5034 females reached the adult stage when reared without the dietary antidote, confirming 100% penetrance of the OX5034 phenotype. Experimental design resulted in the testing of 500 females homozygous with the OX5034 gene and 1000 females hemizygous with the OX5034 gene. Female hemizygous with the OX5034 gene are genetically comparable to the female offspring that would result in the field from OX5034 male releases and therefore, it is important that even with only one copy of the OX5034, 100% female lethality was also confirmed.

Table 5. Crosses for penetrance testing. ‘OX5034’ refers to a homozygous individual (carrying two copies of the transgene). ‘LWT’ refers to an individual without any copy of the transgene. OX5034 crossed to LWT will produce progeny with one copy of the transgene. LWT crosses act as a negative control, with zero copies of the OX5034 transgene. Doxycycline is a tetracycline analogue. This table has been modified from MRID 50889417 to refer to ‘WT’ as ‘LWT.’

Cross	200 L1 larvae in 200 mL doxycycline (4 µg/mL)	200 L1 larvae in 200 mL dl water
OX5034 ♂ x OX5034 ♀	5 repeats	5 repeats
OX5034 ♂ x LWT ♀	5 repeats	5 repeats
OX5034 ♀ x LWT ♂	5 repeats	5 repeats
LWT ♂ x LWT ♀	5 repeats	5 repeats

Field collected eggs from OX5034 releases that occurred outside of the United States were brought into the laboratory, hatched, and reared in the absence of the dietary antidote. The study found complete penetrance of the OX5034 phenotype in the field collected samples, indicating that the OX5034 phenotype still results in female lethality even when the OX5034 trait is expressed in a different genetic background in a geographically distinct population. PCR reactions were also run for a subset of the field collected samples to confirm that surviving females believed to lack the OX5034 cassette based on a lack of fluorescence, did indeed lack the OX5034 cassette (i.e., to confirm that surviving wild-type females were truly wild-type). The results from the studies using mosquitoes from laboratory colonies and from field collections, demonstrate that the OX5034 phenotype is 100% penetrant and that all females containing a copy of the OX5034 trait die prior to adulthood when reared in the absence of a tetracycline analogue.

Environmental sources of tetracycline

Because the presence of tetracycline(s) in the environment may affect survivability of female OX5034 mosquitoes, the likelihood that OX5034 mosquitoes would encounter tetracycline sources at levels high enough for rescue from the lethal phenotype was evaluated. Several lines of evidence including a survey of environmental levels of tetracycline, tetracycline dose-response testing of OX5034 females, and oviposition behavior of *Ae. aegypti*, indicate that the risk of OX5034 female mosquitoes emerging in the environment due to high levels of tetracycline is low. Trial site location restrictions using known *Ae. aegypti* dispersal distances to limit exposure to locations with higher probabilities of containing tetracycline would further reduce the likelihood of OX5034 females in the environment to the point where the risk would be considered negligible.

Tetracyclines in the environment can come from human or animal drugs, or non-drug sources such as in agriculture. The dose-response of OX5034 mosquitoes to a range of tetracycline analogues (doxycycline chlortetracycline, tetracycline, and oxytetracycline) was evaluated to determine what levels are required to rescue female OX5034 mosquitoes (MRID 50889415). These rescue levels were compared to

concentrations of the tetracycline analogues typically found in the environment as a result of industrial or household tetracycline usage in the United States. Environmental concentrations were obtained through a literature search combining USA with the name of each tetracycline analogue and with relevant terms like wastewater, effluent, ground water, or surface water. In all cases the minimum concentration for each analogue required to rescue OX5034 females capable of maintaining flight is higher than the mean concentrations found in environmental water bodies for the studies reviewed. Because tetracycline analogue levels in the environment were found to be lower than the levels needed for OX5034 rescue, there is a low risk of OX5034 mosquitoes encountering levels of tetracycline high enough to result in the emergence of OX5034 females.

The oviposition behavior of *Ae. aegypti* further reduces the likelihood that OX5034 mosquitoes would encounter sources where tetracycline and its analogues may be present. *Ae. aegypti* prefer man-made containers such as gutters, water containers, and tires that hold rainwater or clean still water for their breeding sites [ADDIN EN.CITE ADDIN EN.CITE.DATA]. These containers are unlikely to house significant levels of tetracycline analogues. Female *Ae. aegypti* also lay their eggs at several different sites as opposed to laying them in one breeding container. This oviposition behavior creates a challenge in terms of pest control, but further reduces the likelihood that many eggs would be laid in water containing significant concentrations of tetracycline analogues, should *Ae. aegypti* deviate from their typical breeding site preference.

EPA also considered potential sources of tetracycline analogues specific to the proposed trial areas. Aquaculture facilities, farms, hospitals, or municipal sewage facilities are likely the only sources that theoretically could introduce sufficiently high levels of tetracycline into the environment to allow survival of OX5034 females. Given that the proposed trial areas are likely to be in relatively developed (urbanized) areas due to preferred *Ae. aegypti* habitat, the presence of livestock or aquaculture is not expected. However, because Florida is a major producer of citrus and oxytetracycline applications are being used in citrus groves to combat citrus greening, the applicant has stated that the outer boundary of the trial areas will be greater than 400 m from commercial citrus growing areas to reduce the likelihood that OX5034 mosquitoes could encounter increased levels of oxytetracycline as a result of these applications.

A 2004 survey found that although most mosquito larvae in the Florida Keys were collected from tires, flowerpots, planters, and trivets, some larvae were collected from sewage treatment plants, septic tanks, and cesspits [ADDIN EN.CITE

<EndNote><Cite><Author>Hribar</Author><Year>2004</Year><RecNum>502</RecNum><DisplayText>(Hribar et al. 2004)</DisplayText><record><rec-number>502</rec-number><foreign-keys><key app="EN" db-id="9dafa52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1584548144">502</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Hribar, L. J.</author><author>Vlach, J. J.</author><author>DeMay, D. J.</author><author>James, S. S.</author><author>Fahey, J. S.</author><author>Fussell, E. M.</author></authors></contributors><titles><title>Mosquito larvae (Culicidae) and other Diptera associated with containers, storm drains, and sewage treatment plants in the Florida Keys, Monroe County, Florida</title><secondary-title>Florida Entomologist</secondary-title></titles><periodical><full-title>Florida Entomologist</full-title></periodical><pages>199-203</pages><volume>87</volume><number>2</number><dates><year>2004</year><pub-dates><date>Jun</date></pub-dates></dates><isbn>0015-4040</isbn><accession-num>WOS:000222319500016</accession-num><urls><related-urls><url><Go to ISI>://WOS:000222319500016</url></related-urls></urls><electronic-resource-num>10.1653/0015-4040(2004)087[0199:mlcaod]2.0.co;2</electronic-resource-num></record></Cite></EndNote>].

However, these are not preferred breeding sites and breeding in septic tanks can only occur where the lid is cracked or broken [ADDIN EN.CITE

<EndNote><Cite><Author>Burke</Author><Year>2010</Year><RecNum>501</RecNum><DisplayText>(Burke et al. 2010)</DisplayText><record><rec-number>501</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1584548144">501</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Burke, R.</author><author>Barrera, R.</author><author>Lewis, M.</author><author>Kluchinsky, T.</author><author>Claborn, D.</author></authors></contributors><titles><title>Septic tanks as larval habitats for the mosquitoes *Aedes aegypti* and *Culex quinquefasciatus* in Playa-Playita, Puerto Rico</title><secondary-title>Medical and Veterinary Entomology</secondary-title></titles><periodical><full-title>Medical and Veterinary Entomology</full-title></periodical><pages>117-123</pages><volume>24</volume><number>2</number><dates><year>2010</year><pub-dates><date>Jun</date></pub-dates></dates><isbn>0269-283X</isbn><accession-num>WOS:000277975700003</accession-num><urls><related-urls><url><Go to ISI>://WOS:000277975700003</url></related-urls></urls><electronic-resource-num>10.1111/j.1365-2915.2010.00864.x</electronic-resource-num></record></Cite></EndNote>]. Furthermore, since 2004 Key West and surrounding areas in Monroe County have eliminated most septic tanks and use a public sewer line system as the major means of waste disposal. Most of the County is now served by the Cudjoe Regional Wastewater System that includes a deep injection well, which disposes of treated effluent 3,200 feet below the surface, thus excluding exposure of *Ae. aegypti* to effluent [ADDIN EN.CITE <EndNote><Cite><Author>Monroe County Wastewater Master Plan</Author><RecNum>510</RecNum><Prefix>see web links for </Prefix><Suffix> in references</Suffix><DisplayText>(see web links for City of Key West , Monroe County Wastewater Master Plan in references)</DisplayText><record><rec-number>510</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1584555750">510</key></foreign-keys><ref-type name="Web Page">12</ref-type><contributors><authors><author>Monroe County Wastewater Master Plan,</author></authors></contributors><titles></titles><number>February 26, 2020</number><dates></dates><urls><related-urls><url>http://www.monroecounty-fl.gov/124/Wastewater</url></related-urls></urls></record></Cite><Cite><Author>City of Key West</Author><RecNum>509</RecNum><record><rec-number>509</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1584555666">509</key></foreign-keys><ref-type name="Web Page">12</ref-type><contributors><authors><author>City of Key West,</author></authors></contributors><titles><title>Wastewater Treatment</title></titles><number>January 14, 2020</number><dates></dates><urls><related-urls><url>https://www.cityofkeywest-fl.gov/departments/division.php?structureid=164</url></related-urls></urls></record></Cite></EndNote>]. Each of the Florida Keys Aqueduct Authority Wastewater Districts¹ has its own municipal wastewater treatment facility, which consist of a series of open holding tanks. These open holding tanks could allow access to mosquitoes, although this would not be a preferred breeding site as *Ae. aegypti* prefer to oviposit in clear waters. The likelihood of these tanks containing high enough levels of tetracycline to rescue OX5034 females is also low because tetracycline rapidly undergoes aqueous photolysis in the presence of sunlight. In Harris County, Texas, reclaimed water from all of Houston wastewater plants is discharged directly into a surface waterway, usually one of the area bayous [ADDIN EN.CITE <EndNote><Cite><Author>City of Houston</Author><RecNum>508</RecNum><Prefix>see web link </Prefix><Suffix> in references</Suffix><DisplayText>(see web link City of Houston in references)</DisplayText><record><rec-number>508</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1584555621">508</key></foreign-keys><ref-type name="Web Page">12</ref-type><contributors><authors><author>City of

¹ Navy, Key Haven, Big Coppit, Bay Point, Cudjoe Regional, Duck Key, and Layton Long Key.

Houston, </author></authors></contributors><titles><title>Wastewater FAQs</title></titles><number>January 14, 2020</number><dates></dates><urls><related-urls><url>https://www.publicworks.houstontx.gov/pud/faq.html</url></related-urls></urls></record></Cite></EndNote>]. However, bayous are not typical breeding sites for *Ae. aegypti*. Although the Agency considers it unlikely that these abovementioned sources would have sufficient levels of tetracycline to rescue OX5034 females based on the literature survey, limiting the proximity of trial site locations from any wastewater treatment facility in either Monroe or Harris County would further reduce that likelihood. As release recapture studies around the world have found that a small percentage of *Ae. aegypti* were found 170 m but not more than 200 m from the release point [ADDIN EN.CITE <EndNote><Cite><Author>OECD</Author><Year>2018</Year><RecNum>511</RecNum><DisplayText>(OECD 2018)</DisplayText><record><rec-number>511</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1585148502">511</key></foreign-keys><ref-type name="Book">6</ref-type><contributors><authors><author>OECD</author></authors></contributors><titles><title>Safety Assessment of Transgenic Organisms in the Environment, Volume 8</title></titles><dates><year>2018</year></dates><urls><related-urls><url>https://www.oecd-ilibrary.org/content/publication/9789264302235-en</url></related-urls></urls><electronic-resource-num>doi:https://doi.org/10.1787/9789264302235-en</electronic-resource-num></record></Cite></EndNote>], a similar restriction of 400 m from a wastewater treatment site (200 m for released OX5034 males + 200 m for mated *Ae. aegypti* females) may be warranted.

In addition to the traditional sources of tetracycline discussed above, it has been shown in a laboratory study when OX513A larvae (Oxitec's Generation 1 mosquito) were exclusively fed a chicken-based cat food, some survival to adulthood occurred due to tetracycline contamination [ADDIN EN.CITE <EndNote><Cite><Author>Massonnet-Bruneel</Author><Year>2013</Year><RecNum>106</RecNum><DisplayText>(Massonnet-Bruneel et al. 2013)</DisplayText><record><rec-number>106</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1508245831">106</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Massonnet-Bruneel, B.</author><author>Corre-Catelin, N.</author><author>Lacroix, R.</author><author>Lees, R. S.</author><author>Hoang, K. P.</author><author>Nimmo, D.</author><author>Alphey, L.</author><author>Reiter, P.</author></authors></contributors><titles><title>Fitness of Transgenic Mosquito *Aedes aegypti* Males Carrying a Dominant Lethal Genetic System</title><secondary-title>Plos One</secondary-title></titles><periodical><full-title>Plos One</full-title></periodical><volume>8</volume><number>5</number><dates><year>2013</year><pub-dates><date>May</date></pub-dates></dates><isbn>1932-6203</isbn><accession-num>WOS:000319107400014</accession-num><urls><related-urls><url><Go to ISI>;//WOS:000319107400014</url></related-urls></urls><custom7>e62711</custom7><electronic-resource-num>10.1371/journal.pone.0062711</electronic-resource-num></record></Cite></EndNote>]. However, cat food is not believed to be a plausible source of tetracycline exposure for OX5034 mosquitoes in the environment as it would require that adequate levels of cat food be found in a container to create a high enough concentration of tetracycline and that the container also hold adequate levels of water for mosquitoes and that these conditions are maintained over at least 8-10 days for larval and pupal development.

Finally, the Agency also considered whether degradation products of tetracyclines could impact OX5034 female survival. Limited information is available as to environmental concentrations of these degradation products or how the various degradation products could interact with the tet-off system. However, as these degradation products are products of tetracycline, it is logical to infer that sources believed to have the highest concentrations of tetracycline are also those most likely to have any significant level of

degradation product. Therefore, any restrictions on the location trial area boundaries and wastewater treatment facilities would also reduce uncertainty surrounding degradation products.

Based on known oviposition preference of *Ae. aegypti* and literature surveys of environmental concentrations of tetracycline analogues indicating levels lower than those shown necessary through dose response testing to rescue OX5034 females, the likelihood that OX5034 mosquitoes would encounter tetracycline levels high enough to result in OX5034 females is low. However, maintaining sufficient distance between trial area boundaries and potential tetracycline sources would further increase confidence that there will be no OX5034 females in the trial areas, and reduce uncertainty surrounding potential degradation products. As worldwide release recapture studies indicate maximum dispersal distances of 200 m from the release point [ADDIN EN.CITE

<EndNote><Cite><Author>OECD</Author><Year>2018</Year><RecNum>511</RecNum><DisplayText>(OECD 2018)</DisplayText><record><rec-number>511</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1585148502">511</key></foreign-keys><ref-type name="Book">6</ref-type><contributors><authors><author>OECD</author></authors></contributors><titles><title>Safety Assessment of Transgenic Organisms in the Environment, Volume 8</title></titles><dates><year>2018</year></dates><urls><related-urls><url>https://www.oecd-ilibrary.org/content/publication/9789264302235-en</url></related-urls></urls><electronic-resource-num>doi:https://doi.org/10.1787/9789264302235-en</electronic-resource-num></record></Cite></EndNote>], trial area outer boundaries at least 400 m from these potential tetracycline sources (i.e., citrus groves and wastewater treatment facilities) would greatly reduce remaining uncertainties as this would account for OX5034 male dispersal and mated *Ae. aegypti* dispersal. Therefore, although the likelihood that released OX5034 mosquitoes encounter levels of tetracycline or its analogues high enough to result in the emergence of OX5034 females is low, by further reducing access to these potential tetracycline sources, the likelihood would be reduced to negligible.

b. Human exposure characterization

The risk assessment process for pesticide evaluation is characterized by determining the hazard and exposure to a particular pesticide product using the basic equation: Risk = Hazard x Exposure. Based on this relationship, a pesticide may not exhibit human health risk if it poses either negligible human health hazards and/or negligible human health exposure. A discussion of the potential for human exposure to OX5034 *Ae. aegypti* and its associated traits is provided below.

Dermal exposure

OX5034 *Ae. aegypti* are proposed for environmental releases where they are expected to spread the tTAV-OX5034 and DsRed2-OX5034 traits throughout the local *Ae. aegypti* population. Given this method of pesticide application, the biology of *Ae. aegypti* is an important consideration for evaluating the potential human exposure to OX5034 and associated traits. The dermal route of exposure to tTAV-OX5034 and DsRed2-OX5034 is considered the most relevant were females to be present in the environment, as they could expose humans to both proteins while taking a blood meal (Unit II.B.2.c).

As discussed in Unit II.B.c., at the time the review was completed, no determination on the hazard potential of the tTAV-OX5034 and DsRed2-OX5034 proteins was made. Hazard information is not required, however, to support the current risk assessment of OX5034 due to negligible exposure to female *Ae. aegypti* expressing the tTAV-OX5034 and DsRed2-OX5034 proteins and the resulting negligible human health risks from these individuals (Unit II.B.3.a). Negligible exposure to females is based in part on an analysis of potential oxytetracycline sources in the proposed EUP locations and the subsequent recommendation of spatial separation of OX5034 release sites from commercial citrus growing areas and wastewater treatment sites. These parameters reduce the likelihood that OX5034 mosquitoes could encounter increased levels of oxytetracycline, and consequently, reduces the likelihood of emergence of

female *Ae. aegypti* carrying the OX5034 traits. The geographic restrictions for OX5034 releases are practicable within the scope of this EUP, as ground-truthing of the specific release locations was performed, but not for a full registration under section 3. Thus, the current approach is unlikely to be satisfactory for a registration under FIFRA section 3.

Dermal exposure to male OX5034 was also considered, as they will be released into the environment. Unlike *Ae. aegypti* females, males do not feed on human blood, but rather rely on plant carbohydrates for energy synthesis [ADDIN EN.CITE ADDIN EN.CITE.DATA]. The only plausible route of dermal exposure to male OX5034 is therefore expected to occur via direct (epi-)dermal contact, e.g., upon landing of an adult mosquito on bare skin. Given the different feeding behaviors of male and female *Ae. aegypti*, the frequency of human interaction with male mosquitoes is expected to be minimal. Even if direct skin contact were to occur, because the tTAV-OX5034 and DsRed2-OX5034 proteins as well as the genetic material encoding them are present within the insect's cells, exposure to these substances is expected to be negligible.

Oral exposure

Oral exposure to OX5034 males is expected to be negligible. OX5034 is not proposed for food use, and therefore oral exposure is only conceivable through accidental ingestion of the mosquitoes. As discussed in the dermal exposure section above, exposure to adult female OX5034 is expected to be negligible. The experimental protocol of this EUP proposes releases of both mosquito eggs and adults to evaluate the effects on the local *Ae. aegypti* population. Eggs will be deployed in rearing boxes. Hatching from these release devices is expected to be somewhat asynchronous and to result in a staggered release of adult males. Thus, it is unlikely that at any given time the number of OX5034 males emerging from the rearing box is high enough for accidental ingestion to occur, especially given that handling of these rearing boxes is not required after addition of water to rehydrate the eggs.

Adult male OX5034 releases from vehicles is expected to facilitate dispersal of the mosquitoes in the environment and reduce potential interaction with the applicator to negligible levels. Releases of mosquitoes from containers on foot may result in increased male OX5034 mosquito abundance only at the time and location of application. Because males do not seek out human interaction and are likely to quickly disperse once released, e.g., to find shaded areas and look for food and mating opportunities, the likelihood of accidental ingestion, however, remains low. Males will be released early in adulthood, which is the time when they may not produce any or only low levels of the tTAV-OX5034 protein as it was only detected above the LoD in homozygous male adults 6-days post eclosion, but not at 1-day post eclosion (MRID 50889414). Further, bioinformatics analysis suggests that both tTAV-OX5034 and DsRed2-OX5034 are susceptible to proteolytic degradation in the human gastric system. Furthermore, the cleaved variant of tTAV and a related variant of the DsRed2-OX5034 protein were shown to be labile to simulated gastric fluids *in vitro*. Together, oral exposure to tTAV-OX5034 and DsRed2-OX5034 is expected to be negligible.

Another conceivable route of exposure to tTAV-OX5034 and DsRed2-OX5034 may be through ingestion of water containing OX5034 eggs or larvae that resulted from the matings of OX5034 males and local females. While *Ae. aegypti* is an anthropophilic species, its oviposition sites are not expected to be a source of potable water in the proposed test areas. *Ae. aegypti* is a container-breeding species that is often found to lay eggs in small bodies of water such as puddles, tires, and plants (e.g., leaf axils of bromeliads). Any OX5034 mosquitoes that are present in these bodies of water and that are unable to mature due to the expression of the lethal tTAV-OX5034 protein will be exposed to the normal processes of biodegradation. This expectation is supported by the bioinformatics analysis that predicts susceptibility of the tTAV-OX5034 and DsRed2-OX5034 proteins to the environmental proteases proteinase K and subtilisin. Based on these considerations, it is expected that tTAV-OX5034, DsRed2-OX5034, and the genetic material encoding them are degraded and are unable to reach the ground water, virtually eliminating this route of exposure.

Ocular exposure

Ocular exposure to tTAV-OX5034 and DsRed2-OX5034 and the genetic material encoding them is unlikely, as they are contained within the cells of the insect, which essentially eliminates these exposure routes. The exposure considerations discussed above (i.e., mode of pesticide application, male mosquito behavior once released) in the primary dermal irritation/ acute dermal toxicity, and acute oral toxicity waiver rationales are equally relevant to evaluate the likelihood of ocular exposure. Based on these assessments, ocular exposure to male OX5034 mosquitoes is unlikely to occur. Even if an OX5034 adult male were to accidentally come in contact with the eye, the physical effect from that accidental contact is expected to be minimal and to not be different from those effects resulting from accidental ocular exposure to a wild-type mosquito.

Pulmonary exposure

The exposure considerations discussed above are equally relevant to evaluate the likelihood of pulmonary exposure. Pulmonary exposure to adult OX5034 males is not expected to occur as they are too large to be inhaled, especially into deeper lung tissues [ADDIN EN.CITE

<EndNote><Cite><Author>Gorguner</Author><Year>2010</Year><RecNum>532</RecNum><DisplayText>(Gorguner and Akgun 2010)</DisplayText><record><rec-number>532</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586889080">532</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Gorguner, M.</author><author>Akgun, M.</author></authors></contributors><titles><title>Acute inhalation injury</title><secondary-title>The Eurasian journal of medicine</secondary-title></titles><periodical><full-title>The Eurasian journal of medicine</full-title></periodical><volume>42</volume><number>1</number><section>28</section><dates><year>2010</year></dates><urls></urls></record></Cite></EndNote>]. Pulmonary exposure to adult OX5034 males is not expected to occur as they are too large to be inhaled, especially into deeper lung tissues [ADDIN EN.CITE

<EndNote><Cite><Author>Gorguner</Author><Year>2010</Year><RecNum>532</RecNum><DisplayText>(Gorguner and Akgun 2010)</DisplayText><record><rec-number>532</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586889080">532</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Gorguner, M.</author><author>Akgun, M.</author></authors></contributors><titles><title>Acute inhalation injury</title><secondary-title>The Eurasian journal of medicine</secondary-title></titles><periodical><full-title>The Eurasian journal of medicine</full-title></periodical><volume>42</volume><number>1</number><section>28</section><dates><year>2010</year></dates><urls></urls></record></Cite></EndNote>]. Accidental oral exposure for objects this size is therefore more likely to result in swallowing, i.e., ingestion, rather than inhalation. The circumstances that would allow for the formation and accumulation of airborne particles are not expected to be present at the release sites. Male adult OX5034 will be released into the environment where they seek out females for mating. *Ae. aegypti* oviposition sites will most likely be present outdoors, in areas that are exposed to rain where water can collect. Microbial activity in the environment will facilitate biodegradation of the transgenic proteins and the genetic material present in dead mosquito tissue, which will facilitate removal of these biotic components in the release area over time. Further, male adult mosquitoes are the only adult life stage that carry the OX5034 traits, but only adult females seek out the presence of humans as they rely on the blood meal for egg production. Thus, should access to indoor space be available, the presence of females will not lead to exposure to the tTAV-OX5034 and DsRed2-OX5034 protein or the genetic material encoding them. While it is possible that males may follow females indoors, it is expected to be a rare event that those males would then remain indoors and contribute to dust formation in a significant way. The presence of tTAV-OX5034 and DsRed2-OX5034

proteins and the genetic material encoding them in the insect's cells is expected to reduce the likelihood of pulmonary exposure to overall negligible levels. Information on the charge density of and protein size of tTAV-OX5034 and DsRed2-OX5034 was also considered as part of the exposure evaluation. Neither protein is expected to be able to freely diffuse over cell membranes, which may reduce uptake of these proteins into the lungs. The extent to which these physicochemical characteristics would prevent potential adverse effects is, however, unknown (MRID 50889421).

C. Environmental Fate of the Transgene and OX5034 Background Genetics

1. Introgression data

OX5034 is described as a species-specific female larvicide, or “male-selecting” larvicide, that results in all-male progeny in the absence of tetracyclines in the larval diet due to a female-specific self-limiting gene. With continued field releases of OX5034 homozygous males, the local *Ae. aegypti* population is expected to progressively decline due to the reduced number of females emerging in the area. Specifically, when OX5034 homozygous males are released into the environment and mate with local *Ae. aegypti* females, their offspring inherit a single copy of the self-limiting gene. The self-limiting gene kills only female offspring while hemizygous males survive to pass on the OX5034 self-limiting gene further. As the self-limiting gene is inherited in a Mendelian fashion, half of the offspring resulting from a mating between an OX5034 hemizygous male and a local female would not inherit the self-limiting gene but would still inherit OX5034 background strain genetics. This results in both male and female mosquitoes in the local *Ae. aegypti* population with some degree of OX5034 background strain genetics.

Oxitec, Ltd. submitted scientific rationale, experimental data, modeling studies, and a meta-analysis to address introgression and persistence of the OX5034 transgene and OX5034 background strain genetics into the local *Ae. aegypti* population. A summary of these data is provided in Table 6 and within the risk assessment below. A full review of the rationale is contained within the attached Data Evaluation Records (DERs) except for the study “Introgression of OX5034 Background Genetics.” This study was instead reviewed in the format of an interagency collaborative memo between the EPA and the U.S. Centers for Disease Control and Protection (CDC). Some of the references cited in this assessment were included in rationale provided by the applicant within the MRIDs cited. Other references were included from the open literature that pertained to specific topics discussed below.

Table 6. Status of data submitted to address environmental fate of the OX5034 transgene and OX5034 background genetics.

Study Topic	OPPTS Guideline No.	Results Summary and Classification	MRID No.
OX5034 male-selecting trait decline in a caged population of wild-type <i>Aedes aegypti</i>	N/A	Three experimental caged populations (n=200 individuals per generation per cage) were used to determine how long the OX5034 trait would remain in a wild mosquito population once OX5034 releases ceased. The experiment found that the trait reduced by approx. 54% each generation and disappears from the population in 6-8 generations. Classification: Acceptable.	50889416
Introgression of OX5034 Background Genetics	N/A	A literature review of vectorial capacity and vector competence was combined with a meta-analysis of vector competence data from Florida, data on the OX5034 mosquito (fecundity, longevity), and data from a study on the OX513A mosquito. Classification: Acceptable.	50973401

Modelling the Introgression of OX5034 Background Genetics	N/A	The study aimed to model the degree and persistence of OX5034 background genetic introgression into wild field mosquito populations through use of a deterministic, discrete-generation population genetic model. However, several deficiencies and necessary clarifications make it so the models have limited value. Given that the applicant has characterized the mosquito traits of interest (i.e., characterized the potential hazard), information that could potentially be gleaned from modeling the degree of introgression (i.e., the exposure) is not critical to the risk assessment. Classification: Supplemental.	50973402
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2. Persistence of OX5034 transgene in the environment post-release

The applicant provided an experimental study and a corresponding modeling study to determine the rate at which the introduced OX5034 self-limiting trait will decline in a caged, wild-type *Ae. aegypti* population. The studies are used to indicate how rapidly the OX5034 self-limiting trait will decline and become extinct after the proposed releases of OX5034 male mosquitoes have ceased.

Three replicate caged populations were maintained in the absence of the dietary antidote in the laboratory. Each population was derived from 100 OX5034-hemizygous males crossed to 200 LWT females in a 15 x 15 x 15 cm cage. These populations represent the generation after the final release of OX5034 males under the scenario where all male *Ae. aegypti* mosquitoes remaining in the population are offspring of the released OX5034 males. They also represent the scenario with the highest possible frequency of the OX5034 transgene in the environment because in this scenario there are no wild-type males remaining and all of the males in the population contain a copy of the transgene. During the caged population studies, the frequency of the OX5034 transgene in the population was calculated via proportion of fluorescent pupae for each subsequent generation and graphed over time to show the decline of the OX5034 transgene in the three populations. The applicant also provided a simple stochastic model to predict the decline of the OX5034 transgene where the model assumed complete penetrance of the OX5034 trait and no competitive disadvantage for OX5034 males.

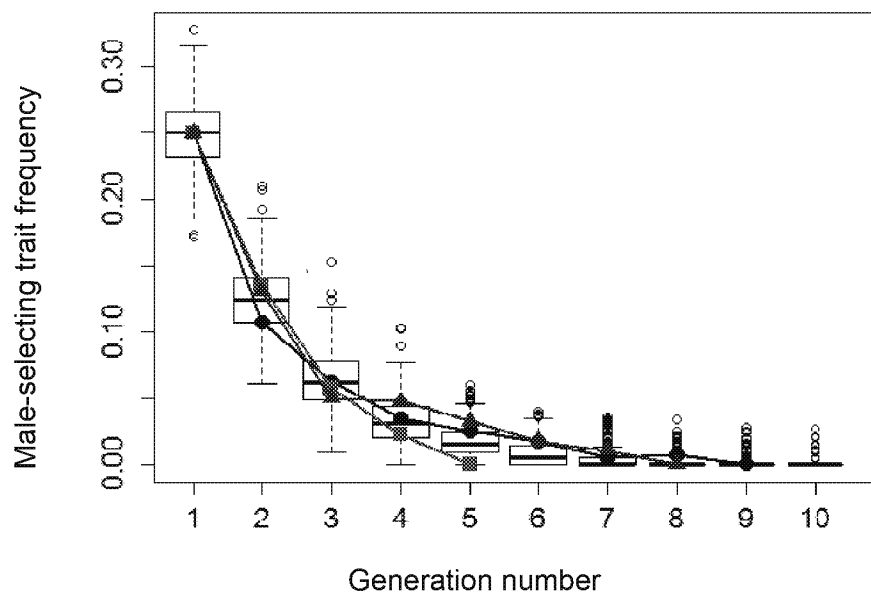


Figure 3. Boxplots showing the results from 500 iterations of a stochastic model simulating the extinction of a male-selecting genetic trait under restrictive conditions. Horizontal bold lines represent generational medians; upper and lower box lines represent first and third quartiles, respectively; outer horizontal lines represent 1.5x the interquartile range; and open circles represent data points over 1.5x above or below the first and third quartiles. Overlaid onto the box plots are lines (red, blue and green) showing male-selecting trait frequency changes from three replicates of caged experiments. Generation 1 represents a post-field release population with a trait frequency of 0.25. Graph and figure legend reproduced from MRID 50889416.

The caged population study found the mean number of generations until disappearance of the OX5034 self-limiting trait across three caged populations to be 7.3 (± 1.2 SE) with 9 being the maximum number of generations until trait disappearance (Figure 3). The model and the starting assumptions predicated that the self-limiting trait frequency would halve in each generation due to the 50% fitness cost of the OX5034 trait (i.e., 100% female lethality). This prediction was observed in the experimental cages, with the average frequency of the self-limiting trait decreasing in each generation by 54% (± 7.0 SE).

Therefore, upon cessation of the proposed OX5034 male releases, it is expected that the OX5034 transgene would disappear from the environment in ~6-8 generations. Furthermore, it is likely that in the field when OX5034 males compete against local *Ae. aegypti* males, the trait will decline faster than found in the modeling and caged population studies, as additional fitness costs associated with the OX5034 trait have been recorded, like reduced egg clutch size in matings with OX5034 homozygous males (Unit II.A.5.c.; MRID 50889417).

3. Introgression of OX5034 background strain genetics

Because the transgene is inherited in a Mendelian fashion and OX5034 hemizygous males are anticipated to survive and contribute to offspring in subsequent generations, it is expected that although the transgene will eventually disappear from the *Ae. aegypti* populations at the proposed release sites, introgression of OX5034 background strain genetics (i.e., genes other than the transgene) will occur. This is because only half of the offspring (both male and female) of an OX5034 hemizygous male would inherit the transgene, resulting in the other half being “wild-type” but still inheriting other OX5034 background strain genetics. Introgression would result in both male and female mosquitoes in the local *Ae. aegypti* population to have some degree of OX5034 background strain genetics, which could increase in frequency after releases have ceased. This is because the releases (if successful in suppressing the population) could result in a population bottleneck once they have ceased, where the founding population is composed of the surviving individuals who likely contain OX5034 background strain genetics due to inundation by OX5034 mosquitoes during releases. This creates the potential to result in an increased frequency of OX5034 background strain genetics in the recovered population, thereby altering the population genetics/traits of the local mosquito population.

A recent paper examining the Oxitec’s 1st generation product, OX513A, found evidence of introgression of the strain’s background genetics after releases in Brazil of males containing the self-limiting tTAV gene [ADDIN EN.CITE

<EndNote><Cite><Author>Evans</Author><Year>2019</Year><RecNum>473</RecNum><DisplayText>(Evans et al. 2019)</DisplayText><record><rec-number>473</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1578060419">473</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Evans, B. R.</author><author>Kotsakiozi, P.</author><author>Costa-da-Silva, A. L.</author><author>Ioshino, R. S.</author><author>Garziera,

L. Pedrosa, M. C. Malavasi, A. Virginio, J. F. Capurro, M. L. Powell, J. R. Transgenic *Aedes aegypti* Mosquitoes Transfer Genes into a Natural Population. *Scientific Reports* 9, 2019, Sep, 2045-2322. WOS:000484988100021. <https://doi.org/10.1038/s41598-019-49660-6>. These findings are relevant to the evaluation of OX5034 because the degree of introgression is likely to be significantly higher than that of the OX513A strain due to differences in larval survival (approx. 5% in OX513A versus 50% in OX5034).

Therefore, given that introgression of OX5034 strain background genetics is expected to occur during releases, it is pertinent to examine potential associated risks for humans and the environment. To do this, EPA evaluated OX5034 mosquitoes for key traits that could increase the ability of mosquitoes to transmit disease, result in larger populations numbers, or result in more robust mosquitoes. As discussed below, based on a combination of laboratory data, meta-analyses, and the large impact of environmental factors on the traits evaluated, EPA believes it is unlikely that the local mosquito population would pose any increased risk to humans or the environment due to releases of OX5034 mosquitoes and introgression of OX5034 background strain genetics under the applied for EUP.

a. Vectorial capacity

As *Ae. aegypti* is a known disease vector, traits associated with vectorial capacity in OX5034 mosquitoes were evaluated. OX5034 mosquitoes were evaluated for resistance to insecticides, as insecticide resistance would result in mosquito populations more difficult to control. Vector competence, or the intrinsic ability of a vector to acquire, maintain, and transmit an infection, was reviewed for *Ae. aegypti* mosquitoes across different geographies and different viruses. Other traits like fecundity and longevity were also reviewed, as increased fecundity could result in larger mosquito populations and increased longevity could increase the likelihood of a mosquito transmitting an infection.

For insecticide resistance, laboratory studies found that OX5034 was susceptible to the pesticide active ingredients Temephos (larvicide), Permethrin, Deltamethrin, and Malathion (three adulticides), and the strain does not carry pyrethroid resistance-associated *kdr* mutations (MRIDs 50698718, 50889418, and 509734-05; discussed in Unit II.A.5.a). While the strain showed some resistance to Propoxur, this chemical is not approved for uses on mosquitoes in the U.S. and thus any resistance associated with Propoxur will not affect current mosquito control practices. For the other traits, EPA, along with CDC, conducted a review of laboratory data, a meta-analysis and rationale submitted by the applicant to compare the vectorial capacity of OX5034 mosquitoes to that of wild mosquitoes. A full review of this topic can be found in the accompanying memo [ADDIN EN.CITE

(USEPA 2020). Summ ary of the Data and Information Related to Vectorial Capacity Presented for the New Product OX5034 (EPA File Symbol: 93167-EUP-E). Memo from Amanda A. Pierce to Eric W. Bohnenblust, dated

February 12,

2020.</title></titles><dates><year>2020</year></dates><urls></urls></record></Cite></EndNote>].

The conclusions of this review are below:

Vectorial capacity is influenced by a number of traits impacted by gene-environment interactions and is confounded by both intrinsic and extrinsic variables. Several traits relevant to vectorial capacity were evaluated for the OX5034 mosquito given the expectation of introgression of OX5034 strain genetics into the local mosquito population.

In terms of introgression of alleles related to vector competence, different populations of the same mosquito species can differ in the likelihood of becoming infected, which can also differ by virus type and even by strains of the same virus. However, vector competence is only partially influenced by genetics, with other known influences coming from abiotic factors, nutrition, microbiota, and larval stage competition. Given the potentially limited role of mosquito genetics in vector competence as well as the known temporal and spatial variation of vector competence among mosquito populations, it is not expected that introgression of OX5034 strain genetics would increase the vector competence of the local mosquito populations.

Fecundity and longevity of the OX5034 mosquito were also evaluated (Unit II.A.5.c and Unit II.A.5.d). Data provided by the applicant combined with literature searches indicate that fecundity and longevity of OX5034 mosquitoes is within the range expected for *Ae. aegypti* and therefore introgression of OX5034 strain genetics is unlikely to result in the increased fecundity or longevity of local mosquitoes.

In conclusion, given the data on insecticide resistance, longevity, and fecundity, the large impact of the environment on all traits evaluated and the complexity of vector competence, EPA believes it is unlikely that the introgression of OX5034 strain genetics would result in increased vectorial capacity of the local mosquito populations under the applied for EUP.

b. Hybrid vigor

EPA also investigated the concepts of “hybrid vigor,” in which the crossbreeding of two different genetic backgrounds results in offspring that are superior to both parents, and the opposite scenario “outbreeding depression,” in which the offspring are less viable. These topics are also reviewed in the accompanying memo [ADDIN EN.CITE

<EndNote><Cite><Author>USEPA</Author><Year>2020</Year><RecNum>526</RecNum><DisplayText>(USEPA 2020)</DisplayText><record><rec-number>526</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1586885155">526</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>USEPA,</author></authors></contributors><titles><title>Summary of the Data and Information Related to Vectorial Capacity Presented for the New Product OX5034 (EPA File Symbol: 93167-EUP-E). Memo from Amanda A. Pierce to Eric W. Bohnenblust, dated February 12,

2020.</title></titles><dates><year>2020</year></dates><urls></urls></record></Cite></EndNote>], but will be restated below.

The Evans et al., 2019 study postulated that releases of the OX513A mosquito in Brazil and the resulting introgression of strain background genetics into the local population “very likely [resulted] in a more robust population than the pre-release population due to hybrid vigor.” The concept of hybrid vigor, or heterosis, is that deleterious alleles persist in populations and that inbreeding due to drift or population isolation results in reduced vigor from increasing homozygosity of deleterious alleles [ADDIN EN.CITE

<EndNote><Cite><Author>Charlesworth</Author><Year>2009</Year><RecNum>485</RecNum><DisplayText>(Charlesworth and Willis 2009)</DisplayText><record><rec-number>485</rec-number><foreign-keys><key app="EN" db-id="9dafa52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1578068355">485</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Charlesworth, D.</author><author>Willis, J. H.</author></authors></contributors><titles><title>The genetics of inbreeding depression</title><secondary-title>Nature Reviews Genetics</secondary-title></titles><periodical><full-title>Nature Reviews Genetics</full-title></periodical><pages>783-796</pages><volume>10</volume><number>11</number><dates><year>2009</year><pub-dates><date>Nov</date></pub-dates></dates><isbn>1471-0056</isbn><accession-num>WOS:000270915400014</accession-num><urls><related-urls><url><Go to ISI>://WOS:000270915400014</url></related-urls></urls><electronic-resource-num>10.1038/nrg2664</electronic-resource-num></record></Cite></EndNote>]. This vigor is restored by crossing individuals of divergent genotypes, resulting in hybrid vigor through rescue from recessive, deleterious alleles. Hybrid vigor is most commonly reported in crossings within domesticated crops and livestock, which is expected given the intense artificial selection and inbreeding depression that takes place in the development of the parental lines. An instance of hybrid vigor was reported in a malaria vectoring mosquito, *Anopheles coluzzii*, but this was found after crossing two inbred laboratory strains, which again, is unsurprising [ADDIN EN.CITE <EndNote><Cite><Author>Ekechukwu</Author><Year>2015</Year><RecNum>484</RecNum><DisplayText>(Ekechukwu et al. 2015)</DisplayText><record><rec-number>484</rec-number><foreign-keys><key app="EN" db-id="9dafa52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1578068355">484</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Ekechukwu, N. E.</author><author>Baeshen, R.</author><author>Traore, S. F.</author><author>Coulibaly, M.</author><author>Diabate, A.</author><author>Catteruccia, F.</author><author>Tripet, F.</author></authors></contributors><titles><title>Heterosis Increases Fertility, Fecundity, and Survival of Laboratory-Produced F-1 Hybrid Males of the Malaria Mosquito *Anopheles coluzzii*</title><secondary-title>G3-Genes Genomes Genetics</secondary-title></titles><periodical><full-title>G3-Genes Genomes Genetics</full-title></periodical><pages>2693-2709</pages><volume>5</volume><number>12</number><dates><year>2015</year><pub-dates><date>Dec</date></pub-dates></dates><isbn>2160-1836</isbn><accession-num>WOS:000367257500019</accession-num><urls><related-urls><url><Go to ISI>://WOS:000367257500019</url></related-urls></urls><electronic-resource-num>10.1534/g3.115.021436</electronic-resource-num></record></Cite></EndNote>]. Although there may be some inbreeding depression in the OX5034 colony due to common lab rearing practices, there is no indication that the local mosquito populations under the proposed EUP are suffering from inbreeding depression. Therefore, there is no indication that matings between OX5034 mosquitoes and local mosquitoes would result in hybrid vigor.

The opposite of inbreeding depression and heterosis would be outbreeding depression. In this instance, genetic incompatibilities like Dobzhansky-Muller incompatibilities result in reduced fitness in hybrids between widely divergent populations or species [ADDIN EN.CITE <EndNote><Cite><Author>Orr</Author><Year>1995</Year><RecNum>494</RecNum><DisplayText>(Orr 1995)</DisplayText><record><rec-number>494</rec-number><foreign-keys><key app="EN" db-id="9dafa52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1579228052">494</key></foreign-

keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Orr, H. A.</author></authors></contributors><titles><title>The population genetics of speciation- the evolution of hybrid incompatibilities</title><secondary-title>Genetics</secondary-title></titles><periodical><full-title>Genetics</full-title></periodical><pages>1805-1813</pages><volume>139</volume><number>4</number><dates><year>1995</year><pub-dates><date>Apr</date></pub-dates></dates><isbn>0016-6731</isbn><accession-num>WOS:A1995QN97500029</accession-num><urls><related-urls><url><Go to ISI>;//WOS:A1995QN97500029</url></related-urls></urls></record></Cite></EndNote>]. If outbreeding depression were to occur, residual population control from male hybrid offspring containing the self-limiting tTAV gene may be reduced due to decreased hybrid fitness, but some level of population control is still expected from initial OX5034 releases. That being said, there is no indication that the OX5034 strain is so divergent from local populations as to expect any significant degree of postzygotic isolation and therefore, there is no indication that matings between OX5034 mosquitoes and local mosquitoes would result in outbreeding depression.

4. Potential for resistance during field releases

Resistance can evolve in response to the OX5034 releases through two primary mechanisms: (1) mosquitoes with the OX5034 trait can evolve genetic resistance resulting in increased larval survival rates and (2) local mosquitoes can evolve behavioral resistance to avoid mating with OX5034 males.

OX5034 *Ae. aegypti* contains a dominant lethal trait, which results from the overproduction of the tTAV-OX5034 protein in female mosquitoes, mediated by a positive feedback loop circuit. The overproduction of the protein is thought to interfere with gene expression within the insect cell through a mechanism called transcriptional squelching [ADDIN EN.CITE ADDIN EN.CITE.DATA]. The level of tTA expression in Tet-OFF systems was shown to be positively correlated with the level of penetrance of the lethal trait in other insects [ADDIN EN.CITE

<EndNote><Cite><Author>Fu</Author><Year>2007</Year><RecNum>81</RecNum><DisplayText>(Fu et al. 2007)</DisplayText><record><rec-number>81</rec-number><foreign-keys><key app="EN" db-id="2t2pdevxize0spe5fsvxsfllfd5zwa2ex2s5" timestamp="1586391004">81</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Fu, G. L.</author><author>Condon, K. C.</author><author>Epton, M. J.</author><author>Gong, P.</author><author>Jin, L.</author><author>Condon, G. C.</author><author>Morrison, N. I.</author><author>Dafa'alla, T. H.</author><author>Alphey, L.</author></authors></contributors><auth-address>Oxitec Ltd, Oxford OX14 4RX, EnglandUniv Oxford, Dept Zool, Oxford OX1 3PS, England</auth-address><titles><title>Female-specific insect lethality engineered using alternative splicing</title><secondary-title>Nature Biotechnology</secondary-title><alt-title>Nat Biotechnol</alt-title></titles><alt-periodical><full-title>Nat Biotechnol</full-title></alt-periodical><pages>353-357</pages><volume>25</volume><number>3</number><keywords><keyword>genetic system</keyword><keyword>autocidal control</keyword><keyword>transformer gene</keyword><keyword>in-vivo</keyword><keyword>fly</keyword><keyword>eradication</keyword><keyword>conservation</keyword><keyword>expression</keyword><keyword>management</keyword><keyword>dominant</keyword></keywords><dates><year>2007</year><pub-dates><date>Mar</date></pub-dates></dates><isbn>1087-0156</isbn><accession-num>WOS:000244748300028</accession-num><urls><related-urls><url><Go to ISI>;//WOS:000244748300028</url></related-

`urls</urls><electronic-resource-num>10.1038/nbt1283</electronic-resource-`
`num><language>English</language></record></Cite></EndNote>].` Thus, mutations affecting the
 efficiency of the OX5034 *Ae. aegypti* gene circuit may result in resistance. Further, epigenetic factors
 have been hypothesized to play a role in resistance development through epigenetic effects [ADDIN
 EN.CITE
`<EndNote><Cite><Author>Knudsen</Author><Year>2020</Year><RecNum>137</RecNum><Display`
`Text>(Knudsen et al. 2020)</DisplayText><record><rec-number>137</rec-number><foreign-keys><key`
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`R.</author><author>Barbour, T. M.</author><author>Bowes, L. M.</author><author>Duncan,`
`J.</author><author>Philpott, E.</author><author>Potter, S.</author><author>Scott, M.`
`J.</author></authors></contributors><auth-address>North Carolina State University.North`
`Carolina State University mjscott3@ncsu.edu.</auth-address><titles><title>Genetic Variation and`
`Potential for Resistance Development to the tTA Overexpression Lethal System in`
`Insects</title><secondary-title>G3 (Bethesda)</secondary-title></titles><periodical><full-title>G3`
`(Bethesda)</full-`
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`resource-num>10.1534/g3.120.400990</electronic-resource-num></record></Cite></EndNote>].`
 However, penetrance of the OX5034 sex-specific lethal trait has been shown to be 100% in OX5034
 homo- and hemizygous individuals of the LWT background as well as in hemizygous individuals
 collected from the field and thus the risk from epigenetic effects is expected to be negligible (Unit
 II.B.3.a.).

Spontaneous mutations naturally occur in organisms and contribute to genetic diversity. While unlikely,
 resistance to the lethal trait may develop through mutations of genetic elements that are associated with
 the function of the positive feedback loop gene circuit, thereby lowering the production of *tTAV-OX5034*
 below a tolerance threshold. The genetic circuit engineered into OX5034 *Ae. aegypti* exploits the
 endogenous transcriptional machinery of the mosquito, such as the pre-mRNA splicing machinery.
 Mutations in these conserved parts of the cellular machinery would carry a high fitness cost for the
 individual as other essential functions of the cell would likely also be affected. Additionally, only a subset
 of mutations in the genetic cassette, would have the potential to affect the function of the positive
 feedback loop in a meaningful way. For example, some mutations may be silent in that they do not
 change the amino acid sequence of *tTAV-OX5034* and others may occur in parts of the *tTAV-OX5034*
 gene that are unlikely to negatively affect the positive feedback loop, e.g., within linker sequences or the
 N-terminus of UBQ. The company reports that genetic resistance to the OX5034 trait has not been
 observed in 27 generation equivalence of OX5034 and as part of the field releases involving over 12
 million OX5034 homozygous males. Together, the likelihood for genetic resistance to occur during field
 releases is negligible.

Although uncommon, resistance through assortative mating where local females preferentially mate with
 local males rather than modified males has been reported in other modified insect release programs (e.g.,

sterile insect technique programs). In these instances, this has typically been linked to a loss of quality in the mass-reared insects where local females do not mate with “lesser-quality” males, thereby resulting in a reduction of product efficacy. Loss of quality in mass-reared insects can be reversed by increasing genetic diversity through outbreeding. However, there is an instance of resistance via assortative mating in melon flies that was not linked to a decline in mass-reared insect quality [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Existing variation in female preference coupled with strong selective pressure for females who preferentially mated with local males led to a change in mating preference in this population. In this instance, increasing the number of modified male melon flies overcame the resistance in local females [ADDIN EN.CITE

<EndNote><Cite><Author>Koyama</Author><Year>2004</Year><RecNum>218</RecNum><DisplayText>(Koyama et al. 2004)</DisplayText><record><rec-number>218</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1509128251">218</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Koyama, J.</author><author>Kakinohana, H.</author><author>Miyatake, T.</author></authors></contributors><titles><title>Eradication of the melon fly, *Bactrocera cucurbitae*, in Japan: Importance of behavior, ecology, genetics, and evolution</title><secondary-title>Annual Review of Entomology</secondary-title></titles><periodical><full-title>Annual Review of Entomology</full-title></periodical><pages>331-349</pages><volume>49</volume><dates><year>2004</year></dates><isbn>0066-4170</isbn><accession-num>WOS:000188826400015</accession-num><urls><related-urls><url><Go to ISI>;//WOS:000188826400015</url></related-urls></urls><electronic-resource-num>10.1146/annurev.ento.49.061802.123224</electronic-resource-num></record></Cite></EndNote>].

There is evidence of rapid evolution in mating preference of *Ae. aegypti* mosquitoes [ADDIN EN.CITE ADDIN EN.CITE.DATA], indicating that the potential for resistance through changes in mating preference is possible for this species. However, if behavioral resistance were to evolve, the impact on humans or non-target organisms would be negligible as this would not result in any new risk or exposure scenario and would instead theoretically result in decreased efficacy of the OX5034 releases through lack of successful matings. The theoretical reduction in efficacy would not pose an increased risk from nuisance biting or disease vectoring from the local *Ae. aegypti* population because similar mosquito abatement activity will occur in both treated and untreated areas during the proposed EUP.

The continued mosquito abatement activity can also play a role in combating resistance. By using a combination of mosquito control efforts, this creates a scenario in which the target population faces a greater variation in selection pressures [ADDIN EN.CITE

<EndNote><Cite><Author>Leftwich</Author><Year>2016</Year><RecNum>184</RecNum><DisplayText>(Leftwich et al. 2016)</DisplayText><record><rec-number>184</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1508776931">184</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Leftwich, P. T.</author><author>Bolton, M.</author><author>Chapman, T.</author></authors></contributors><titles><title>Evolutionary biology and genetic techniques for insect control</title><secondary-title>Evolutionary Applications</secondary-title></titles><periodical><full-title>Evolutionary Applications</full-title></periodical><pages>212-230</pages><volume>9</volume><number>1</number><dates><year>2016</year><pub-dates><date>Jan</date></pub-dates></dates><isbn>1752-4571</isbn><accession-

num>WOS:000368250500014</accession-num><urls><related-urls><url><Go to ISI>://WOS:000368250500014</url></related-urls></urls><electronic-resource-num>10.1111/eva.12280</electronic-resource-num></record></Cite></EndNote>]. This strategy can give rise to more sustainable pest control over the long term, as the selection pressure for resistance is weaker and presented as a moving target. Additionally, the combination approach ensures that mosquitoes are killed even if they are resistant to one of the approaches applied.

D. Environmental Effects Assessment

1. Ecological effects data

Oxitec, Ltd. submitted scientific rationale to fulfill most non-target organism data requirements for the proposed EUP. The applicant also conducted studies to support a conclusion of no adverse effect to freshwater fish or freshwater invertebrates. A summary of these data is provided in Table 7 and within the risk assessment below, and full review of the rationale is contained within the attached Data Evaluation Records (DERs). Some of the references cited in this assessment were included in rationale provided by the applicant within the MRIDs cited. Other references were included from the open literature that pertained to specific topics discussed below.

Table 7. Status of data submitted to comply with nontarget organism data requirements published in 40 CFR § 158.2060.

Data Requirement	OPPTS Guideline No.	Results Summary and Classification	MRID No.
Avian Acute Oral Toxicity Avian Dietary Toxicity Wild Mammal Toxicity Terrestrial Plant Toxicity (Seedling Emergence) Terrestrial Plant Toxicity (Vegetative Vigor) Nontarget Insect Testing	850.2100 850.2200 850.2400 850.4100 850.4150 880.4350	Rationale submitted provides sufficient information to determine that toxicity of OX5034 mosquitoes to nontarget organisms is not expected for this use based on limited exposure and lack of sequence homology of OX5034 rDNA proteins to known mammalian toxins. Rationale submitted also provides sufficient information regarding the role of <i>Ae. aegypti</i> in ecosystem food webs (e.g., food source, pollinator) to determine that indirect impacts of OX5034 mosquitoes are negligible. Classification: Acceptable.	50889409 50889410 50889422 50889411 50889412 50889413
Freshwater Invertebrate, LC ₅₀	850.1010	In a 96-hour flow through acute toxicity study, American signal crayfish (<i>Pacifastacus leniusculus</i>) were fed OX5034 mosquitoes daily at a rate of 700 g mosquito larvae/kg-diet. No mortality or adverse sub-lethal effects were observed. No hazard to freshwater invertebrates is expected. Classification: Acceptable.	50698707 50889407
Fish Acute Oral Toxicity, Freshwater	850.1075	In a 14-day semi static-renewal acute toxicity study, guppies (<i>Poecilia reticulata</i>) were fed OX5034 mosquitoes daily at a rate of 700 g mosquito larvae/kg-diet. No mortality or adverse effects were observed. No hazard to freshwater fish is expected. Classification: Acceptable.	50698708, 50889408
Endangered Species Assessment	N/A	A literature review was provided as an analysis of the potential impact of OX5034 <i>Aedes aegypti</i> on threatened and endangered species or critical habitat. Classification: Acceptable.	50889414

2. Ecological exposure and risk characterization

The pesticidal effect of OX5034 is species-specific as it only effects the reproductive success of *Ae. aegypti* through mating between OX5034 *Ae. aegypti* males and local *Ae. aegypti* females that are already present in the release area. With continued field releases of OX5034 homozygous males, the number of *Ae. aegypti* in the treatment area is thought to progressively decline due to the reduced number of females emerging at each consecutive generation. There is also the potential for OX5034 mosquitoes to be released on an area-wide scale, which could result in population level decline of *Ae. aegypti*. Possible adverse effects to non-target organisms from OX5034 releases are two-pronged: direct effects from oral consumption of OX5034 mosquitoes and indirect effects on ecosystem processes from reduced *Ae. aegypti* populations. Both possibilities are evaluated in this risk assessment. To understand the potential exposure to non-target organisms by OX5034 mosquitoes as well as to understand potential indirect impacts of their continued release, a review of basic *Ae. aegypti* biology is presented.

Originating in sub-Saharan Africa, *Ae. aegypti* is believed to have been introduced to the Americas in the 17th century [ADDIN EN.CITE

<EndNote><Cite><Author>Powell</Author><Year>2013</Year><RecNum>67</RecNum><DisplayText>(Nelson 1986, Powell and Tabachnick 2013)</DisplayText><record><rec-number>67</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1507919411">67</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Powell, J. R.</author><author>Tabachnick, W. J.</author></authors></contributors><titles><title>History of domestication and spread of Aedes aegypti - A Review</title><secondary-title>Memorias Do Instituto Oswaldo Cruz</secondary-title></titles><periodical><full-title>Memorias Do Instituto Oswaldo Cruz</full-title></periodical><pages>11-17</pages><volume>108</volume><dates><year>2013</year><pub-dates><date>Dec</date></pub-dates></dates><isbn>0074-0276</isbn><accession-num>WOS:000330037800003</accession-num><urls><related-urls><url><Go to ISI>://WOS:000330037800003</url></related-urls></urls><electronic-resource-num>10.1590/0074-0276130395</electronic-resource-num></record></Cite><Cite><Author>Nelson</Author><Year>1986</Year><RecNum>69</RecNum><record><rec-number>69</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1507922481">69</key></foreign-keys><ref-type name="Book">6</ref-type><contributors><authors><author>Nelson, M.J.</author></authors><secondary-authors><author>Organizaion PAH</author></secondary-authors></contributors><titles><title><style face="italic" font="default" size="100%">Aedes aegypti</style><style face="normal" font="default" size="100%">: Biology and Ecology</style></title></titles><dates><year>1986</year></dates><pub-location>Washington, D.C.</pub-location><urls></urls></record></Cite></EndNote>]. While *Ae. aegypti* historically bred in tree holes and other phytotelmata, it is now well adapted to humans, flourishes in urban areas, and can breed in a number of artificial containers. After mating, female *Ae. aegypti* produce a batch of 100 to 200 eggs and lay their eggs at several different breeding containers. Larval and pupal development occur in these breeding containers, completing the life cycle with adult emergence.

Typical larval habitats include stagnant water with organic matter and can range from tree holes and rock pools to bottle caps and tires [ADDIN EN.CITE ADDIN EN.CITE.DATA]. *Aedes aegypti* usually uses man-made containers such as gutters, water containers, cans, and tires as breeding sites. The use of these containers as a larval habitat reduces the risk of exposure to non-target organisms, thereby reducing the risk of any direct adverse effect on non-targets. In terms of indirect effects, such as ecosystem impacts from a reduction of the local *Ae. aegypti* population as a result of OX5034 releases, *Ae. aegypti* is a non-

native species in the U.S. and has therefore not likely co-evolved with other organisms in the ecosystem and does not represent a keystone species on which other organisms rely for biological processes [ADDIN EN.CITE

<EndNote><Cite><Author>Juliano</Author><Year>2005</Year><RecNum>28</RecNum><DisplayText>(Juliano and Lounibos 2005)</DisplayText><record><rec-number>28</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1507738564">28</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Juliano, S. A.</author><author>Lounibos, L. P.</author></authors></contributors><titles><title>Ecology of invasive mosquitoes: effects on resident species and on human health</title><secondary-title>Ecology Letters</secondary-title></titles><periodical><full-title>Ecology Letters</full-title></periodical><pages>558-574</pages><volume>8</volume><number>5</number><dates><year>2005</year><pub-dates><date>May</date></pub-dates></dates><isbn>1461-023X</isbn><accession-num>WOS:000228397000012</accession-num><urls><related-urls><url><Go to ISI>;//WOS:000228397000012</url></related-urls></urls><electronic-resource-num>10.1111/j.1461-0248.2005.00755.x</electronic-resource-num></record></Cite></EndNote>].

Although the likelihood of *Ae. aegypti* playing a major ecological role is low, mosquitoes can play a number of roles in the environment such as pollinator, detritivore, or food source. These roles can also be relatively diverse as the mosquito life cycle spans both aquatic and terrestrial habitats. Larvae live in water and they can act as food for other aquatic organisms. Mosquito larvae themselves eat microscopic matter like decaying leaves and other organic detritus. As adults, mosquitoes make up part of the diet of some insect-eating animals, such as birds, bats, adult dragonflies, or spiders. However, most mosquito predator species are generalist feeders that do not depend on the presence of any single prey species for survival. In addition to acting as a food source to other organisms, mosquitoes may also act as pollinators due to their consumption of nectar. Each of these points is discussed in further detail in the below subsections.

a. Terrestrial Animals and Plants

Birds and Mammals

Birds and wild mammals will be exposed to OX5034 mosquitoes primarily through ingestion of OX5034 adults and larvae as prey. Based upon bioinformatic analyses, neither DsRed2-OX5034 or tTAV-OX5034 are known to share significant sequence homology with known toxins (MRID 50889420). Both of these proteins are predicted as susceptible to several proteases found in the human gastric system (*i.e.* pepsin, trypsin, chymotrypsin) based upon bioinformatics analysis (MRID 50889420), and thus proteins are expected to be broken down following ingestion. Based upon bioinformatics analyses, both DsRed2-OX5034 and tTAV-OX5034 are also predicted as susceptible to two environmental proteases (*i.e.* proteinase K and subtilisin A) and are thus expected to degrade under field conditions. While several variants of DsRed can sometimes exhibit toxic effects when expressed within living cells, oral consumption and subsequent digestion would result in protein degradation thereby making uptake of the intact protein into cells following ingestion unlikely. Because biting females will not be released, wild birds and mammals will not serve as bloodmeals for mosquitoes carrying tTAV-OX5034 and DsRed2-OX5034 proteins, thus excluding this as an exposure pathway to these proteins. Therefore, direct adverse effects are not expected in birds or wild mammals as a result of release of OX5034 male mosquitoes.

Because OX5034 mosquitoes have the potential to be used on an area-wide scale to suppress local *Ae. aegypti* mosquito populations, it is possible that birds or wild mammals could be indirectly affected

through the reduction of *Ae. aegypti* as a food source. Several types of birds including most varieties of swallows, warblers and other songbirds consume mosquitoes among other flying insects. However, the mosquito is likely to form only a small part of the bird diet. Barn swallows for instance, feed at lower heights where mosquitoes are more likely to fly, but due to the small size of the mosquito, they instead tend to prefer larger insects such as flies or dragonflies. Perhaps the most frequently anecdotally cited bird as a consumer of mosquitoes is the Purple Martin (*Progne subis*), the largest species of martin in North America. However, a study in Oklahoma evaluating prey captured by Purple Martins at various altitudes failed to detect mosquitoes as part of prey fed to young birds [ADDIN EN.CITE

nestlings indicated 51% and 49%, respectively, contained *Aedes* as prey, the study did not provide an indication as to the proportion of the diet that *Aedes* comprised. Conversely, stomach content analyses in another study did not note *Aedes* as a food item for Western Bluebirds. [ADDIN EN.CITE

<EndNote><Cite

AuthorYear="1"><Author>Jedlicka</Author><Year>2017</Year><RecNum>497</RecNum><DisplayText>Jedlicka et al. (2017)</DisplayText><record><rec-number>497</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1583420896">497</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Jedlicka, J. A.</author><author>Vo, A. T.

E.</author><author>Almeida, R. P. P.</author></authors></contributors><titles><title>Molecular scatology and high-throughput sequencing reveal predominately herbivorous insects in the diets of adult and nestling Western Bluebirds (*Sialia mexicana*) in California vineyards</title><secondary-title>Auk</secondary-title></titles><periodical><full-title>Auk</full-title></periodical><pages>116-127</pages><volume>134</volume><number>1</number><dates><year>2017</year><pub-dates><date>Apr</date></pub-dates></dates><isbn>0004-8038</isbn><accession-num>WOS:000392206100011</accession-num><urls><related-urls><url><Go to ISI>://WOS:000392206100011</url></related-urls></urls><electronic-resource-num>10.1642/auk-16-103.1</electronic-resource-num></record></Cite></EndNote>] hypothesizes that a difference in habitat (vineyard vs. woodland) and the generalist nature of bluebird foraging is a likely explanation for the high frequency of detection of *Aedes* in the Western Bluebird diet found in vineyards compared to other studies.

Insectivorous bats are often anecdotally regarded to be a significant predator of mosquitoes and are thought to eat large quantities of mosquitoes. However, in areas where larger, more nutritious insect prey are available, bats do not consume large numbers of mosquitoes as they do not constitute significant calories or nutrients relative to the task of predating upon them [ADDIN EN.CITE ADDIN EN.CITE.DATA]. For example, a study examining the fecal pellets for the little brown bat found that their natural diet was composed of only 1.8% mosquitoes [ADDIN EN.CITE

<EndNote><Cite><Author>Whitaker</Author><Year>1992</Year><RecNum>165</RecNum><DisplayText>(Whitaker and Lawhead 1992)</DisplayText><record><rec-number>165</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1508442432">165</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Whitaker, J. O.</author><author>Lawhead,

B.</author></authors></contributors><titles><title>Foods of *Myotis lucifugus* in a maternity colony in central Alaska</title><secondary-title>Journal of Mammalogy</secondary-title></titles><periodical><full-title>Journal of Mammalogy</full-title></periodical><pages>646-648</pages><volume>73</volume><number>3</number><dates><year>1992</year><pub-dates><date>Aug</date></pub-dates></dates><isbn>0022-2372</isbn><accession-num>WOS:A1992JK33600026</accession-num><urls><related-urls><url><Go to ISI>://WOS:A1992JK33600026</url></related-urls></urls><electronic-resource-num>10.2307/1382037</electronic-resource-num></record></Cite></EndNote>] and the diet of the big brown bat was dominated by beetles and caddisflies. Under certain conditions, such as colder nights where larger insects were less available or when female bats are lactating, Diptera, including mosquitoes and crane flies, may constitute a larger portion of the diet of the southeastern brown bat, *Myotis austroriparius*, in Florida [ADDIN EN.CITE

<EndNote><Cite><Author>Zinn</Author><Year>1981</Year><RecNum>507</RecNum><DisplayText>(Zinn and Humphrey 1981)</DisplayText><record><rec-number>507</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1584555190">507</key></foreign-keys><ref-type name="Journal Article">17</ref-

type><contributors><authors><author>Zinn, T.L.</author><author>Humphrey, S.R.</author></authors></contributors><titles><title><style face="normal" font="default" size="100%">Seasonal Food Resources and Prey Selection of the Southeastern Brown Bat </style><style face="italic" font="default" size="100%">Myotis austroriparius</style><style face="normal" font="default" size="100%"> in Florida USA</style></title><secondary-title>Florida Scientist</secondary-title></titles><periodical><full-title>Florida Scientist</full-title></periodical><pages>81-90</pages><volume>44</volume><dates><year>1981</year></dates><urls></urls><electronic-resource-num>10.2307/24319689</electronic-resource-num></record></Cite></EndNote>]. However, the diversity of the diet of this insectivorous bat increased considerably during warmer temperatures (*i.e.*, most spring and summer nights like when OX5034 releases are proposed). In conclusion, indirect adverse effects such as a reduction in an important food source are not expected in birds or wild mammals as a result of release of OX5034 male mosquitoes.

Nontarget Insects

As *Ae. aegypti* usually use man-made containers such as gutters, water containers, cans, and tires as breeding sites, there is reduced risk of exposure to non-target insects and reduced likelihood that non-target insects specialize in *Ae. aegypti* larvae as a food source. Dragonflies are known to eat adult mosquitoes; however, they also consume butterflies, moths and smaller dragonflies which serve as significant energy sources. Due to this large variety of food sources and the relative lack of energy provided by mosquito consumption, mosquitoes are likely not an essential part of their diet [ADDIN EN.CITE

<EndNote><Cite><Author>Pfitzner</Author><Year>2015</Year><RecNum>166</RecNum><DisplayText>(Pfitzner et al. 2015)</DisplayText><record><rec-number>166</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1508448111">166</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Pfitzner, W. P.</author><author>Beck, M.</author><author>Weitzel, T.</author><author>Becker, N.</author></authors></contributors><titles><title>The role of mosquitoes in the diet of adult dragon and damselflies (Odonata)</title><secondary-title>Journal of the American Mosquito Control Association</secondary-title></titles><periodical><full-title>Journal of the American Mosquito Control Association</full-title></periodical><pages>187-189</pages><volume>31</volume><number>2</number><dates><year>2015</year><pub-dates><date>Jun</date></pub-dates></dates><isbn>8756-971X</isbn><accession-num>WOS:000357707000011</accession-num><urls><related-urls><url><Go to ISI>://WOS:000357707000011</url></related-urls></urls></record></Cite></EndNote>].

Concerns regarding oral consumption of OX5034 mosquitoes by insect species is not considered as a significant risk due to a lack of plausible toxicity to these species via uptake during normal digestive processes. Digestive processes would be expected to degrade proteins, including tTAV-OX5034 and DsRed2-OX5034, as part of the typical acid and enzymic hydrolysis of proteins.

The risk of transfer of the OX5034 cassette to other insect species through mating with OX5034 mosquitoes is highly unlikely as mating in mosquitoes is species specific and depends on time of day, swarming behavior, and wing beat/tone matching. *Ae. aegypti* and *Ae. albopictus* share similar mating habitats and behaviors and therefore the risk of transfer of the OX5034 cassette is likely highest between these two species. However, forced laboratory matings between *Ae. aegypti* and *Ae. albopictus* yielded

eggs that were not viable [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Therefore, the likelihood of transfer of the OX5034 cassette to other insect species is low.

The risk of transfer of OX5034 background strain genetics to local *Ae. aegypti* mosquito populations was also considered. The potential for introgression along with an evaluation of key mosquito traits are discussed in Unit II.C.3. and was determined to be of negligible risk.

Nontarget Plants

Although female *Ae. aegypti* mosquitoes take blood meals from humans, mosquitoes of both sexes require plant juices as an energy source. Therefore, OX5034 male mosquitoes are likely to encounter plants during the experimental releases. Floral nectaries are the best- known sources of sugars and amino acids for insect pollinators, but mosquitoes are also known to obtain sugars from extra- floral nectaries, damaged fruits, damaged and intact vegetative tissues, and honeydew [ADDIN EN.CITE

<EndNote><Cite><Author>Clements</Author><Year>2000</Year><RecNum>134</RecNum><DisplayText>(Clements 2000)</DisplayText><record><rec-number>134</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1508260882">134</key></foreign-keys><ref-type name="Book Section">5</ref-type><contributors><authors><author>Clements,

A.N.</author></authors></contributors><titles><title>Nutrition and reproduction</title><secondary-title>The biology of mosquitoes</secondary-

title</titles><volume>1</volume><edition>2nd</edition><dates><year>2000</year></dates><pub-location>Oxford</pub-location><publisher>CABI

Publishing</publisher><urls></urls></record></Cite></EndNote>]. *Ae. aegypti* are adapted to domestic and urban environments that tend to be low in sugar sources but allow easy and unlimited access to blood meals, such as those around human habitations. It is likely that *Ae. aegypti* males are reliant on sugar sources from potted plants or plant species that are found around houses [ADDIN EN.CITE

<EndNote><Cite><Author>Martinez-Ibarra</Author><Year>1997</Year><RecNum>143</RecNum><DisplayText>(Martinez-Ibarra et al. 1997)</DisplayText><record><rec-number>143</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1508428003">143</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Martinez-Ibarra,

J. A.</author><author>Rodriguez, M. H.</author><author>Arredondo-Jimenez, J.

I.</author><author>Yuval, B.</author></authors></contributors><titles><title>Influence of plant abundance on nectar feeding by *Aedes aegypti* (Diptera : Culicidae) in southern

Mexico</title><secondary-title>Journal of Medical Entomology</secondary-title></titles><periodical><full-title>Journal of Medical Entomology</full-title></periodical><pages>589-593</pages><volume>34</volume><number>6</number><dates><year>1997</year><pub-dates><date>Nov</date></pub-dates></dates><isbn>0022-2585</isbn><accession-num>WOS:000071212100002</accession-num><urls><related-urls><url><Go to ISI>://WOS:000071212100002</url></related-urls></urls></record></Cite></EndNote>]. However,

given that DsRed2-OX5034 and tTAV-OX5034 are expressed in OX5034 tissues within the confines of its chitinous exoskeleton, both proteins are unavailable to plants therefore resulting in negligible exposure.

There is limited information on the pollination of plant species by mosquitoes in general, though related

Aedes spp. are known pollinators of the orchid species *Platanthera obtusata*, which is widely distributed across the Pacific Northwest, around the Great Lakes, and in parts of New England [ADDIN EN.CITE

<EndNote><Cite><Author>Clements</Author><Year>2000</Year><RecNum>134</RecNum><DisplayText>(Clements 2000)</DisplayText><record><rec-number>134</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1508260882">134</key></foreign-keys><ref-type name="Book Section">5</ref-type><contributors><authors><author>Clements,

A.N.</author></authors></contributors><titles><title>Nutrition and reproduction</title><secondary-title>The biology of mosquitoes</secondary-title></titles><volume>1</volume><edition>2nd</edition><dates><year>2000</year></dates><pub-location>Oxford</pub-location><publisher>CABI Publishing</publisher><urls></urls></record></Cite></EndNote>]. However, given that DsRed2-OX5034 and tTAV-OX5034 are expressed in OX5034 tissues within the confines of its chitinous exoskeleton, both proteins are unavailable to plants therefore resulting in negligible exposure.

There is limited information on the pollination of plant species by mosquitoes in general, though related *Aedes spp.* are known pollinators of the orchid species *Platanthera obtusata*, which is widely distributed across the Pacific Northwest, around the Great Lakes, and in parts of New England [ADDIN EN.CITE

<EndNote><Cite><Author>Thien</Author><Year>1969</Year><RecNum>141</RecNum><DisplayText>(Thien 1969, Gorham 1976)</DisplayText><record><rec-number>141</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1508427763">141</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Thien, L.B.</author></authors></contributors><titles><title><style face="normal" font="default" size="100%">Mosquito pollination of</style><style face="italic" font="default" size="100%">Habenaria obtusata</style><style face="normal" font="default" size="100%">(Orchidaceae)</style></title><secondary-title>American Journal of Botany</secondary-title></titles><periodical><full-title>American Journal of Botany</full-title></periodical><pages>6</pages><volume>56</volume><section>232</section><dates><year>1969</year></dates><urls></urls></record></Cite><Cite><Author>Gorham</Author><Year>1976</Year><RecNum>144</RecNum><record><rec-number>144</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1508428003">144</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Gorham, J. R.</author></authors></contributors><titles><title>Orchid pollination by Aedes mosquitoes in Alaska</title><secondary-title>American Midland Naturalist</secondary-title></titles><periodical><full-title>American Midland Naturalist</full-title></periodical><pages>208-210</pages><volume>95</volume><number>1</number><dates><year>1976</year></dates><isbn>0003-0031</isbn><accession-num>WOS:A1976BF88900022</accession-num><urls><related-urls><url><Go to ISI>;//WOS:A1976BF88900022</url></related-urls></urls><electronic-resource-num>10.2307/2424249</electronic-resource-num></record></Cite></EndNote>]. There are no reports that *Ae. aegypti* is a pollinator for any plant species but a laboratory study demonstrated that *Ae. aegypti* is attracted to the scent of the orchid *P. obtusata* and thus is physiologically capable of being a pollinator for this plant [ADDIN EN.CITE

<EndNote><Cite><Author>Lahondere</Author><Year>2020</Year><RecNum>495</RecNum><DisplayText>(Lahondere et al. 2020)</DisplayText><record><rec-number>495</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1583266252">495</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Lahondere, C.</author><author>Vinauger, C.</author><author>Okubo, R. P.</author><author>Wolff, G. H.</author><author>Chan, J. K.</author><author>Akbari, O. S.</author><author>Riffell, J. A.</author></authors></contributors><titles><title>The olfactory basis of orchid pollination by mosquitoes</title><secondary-title>Proceedings of the National Academy of Sciences of the United States of America</secondary-title></titles><periodical><full-title>Proceedings of the National Academy of Sciences of the United States of America</full-title></periodical><pages>708-716</pages><volume>117</volume><number>1</number><dates><year>2020</year><pub-dates><date>Jan</date></pub-dates></dates><isbn>0027-8424</isbn><accession-num>WOS:000506001200095</accession-num><urls><related-urls><url><Go to ISI>;//WOS:000506001200095</url></related-urls></urls><electronic-resource-num>10.1073/pnas.1910589117</electronic-resource-num></record></Cite></EndNote>]. It is important to note that *P. obtusata* is found outside of the experimental permit area, although even if it were found in the experimental permit area, it is highly unlikely that *P. obtusata* would be reliant on *Ae. aegypti* as a primary pollinator because, as a non-native species, the mosquito has not been present in the ecosystem for sufficient time to develop an essential ecosystem function. Dedicated pollinator species for particular flowers require close evolution for many thousands of years [ADDIN EN.CITE

<EndNote><Cite><Author>Patiny</Author><Year>2012</Year><RecNum>142</RecNum><DisplayText>

xt>(Patiny 2012)</DisplayText><record><rec-number>142</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1508427838">142</key></foreign-keys><ref-type name="Book">6</ref-type><contributors><authors><author>Patiny, S.</author></authors></contributors><titles><title>Evolution of plant-pollinator relationships</title></titles><dates><year>2012</year></dates><pub-location>Cambridge</pub-location><publisher>Cambridge University Press</publisher><urls></urls></record></Cite></EndNote>]. Therefore, due to the lack of dedicated pollinator activity by *Ae. aegypti*, any reduction in the local mosquito population as a result of OX5034 male releases is not expected to adversely impact plant populations.

b. Aquatic Animals and Plants

Freshwater, Marine/Estuarine Fish, and Invertebrates and Aquatic Plants

Aquatic organisms which feed on mosquitoes are regarded as generalized predators. Aquatic invertebrate predators, such as larvae from the Coleoptera (beetles), Diptera (flies), Hemiptera (true bugs), and Odonata (dragonflies) orders are known to prey on mosquito larvae [ADDIN EN.CITE <EndNote><Cite><Author>Shaalán</Author><Year>2009</Year><RecNum>146</RecNum><Display Text>(Shaalán and Canyon 2009)</DisplayText><record><rec-number>146</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1508433070">146</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Shaalán, E. A. S.</author><author>Canyon, D. V.</author></authors></contributors><titles><title>Aquatic insect predators and mosquito control</title><secondary-title>Tropical Biomedicine</secondary-title></titles><periodical><full-title>Tropical Biomedicine</full-title></periodical><pages>223-261</pages><volume>26</volume><number>3</number><dates><year>2009</year><pub-dates><date>Dec</date></pub-dates></dates><isbn>0127-5720</isbn><accession-num>WOS:000274667600001</accession-num><urls><related-urls><url><Go to ISI>://WOS:000274667600001</url></related-urls></urls></record></Cite></EndNote>]. Mosquitoes themselves are known to prey on the larvae of other species. For example, *Toxorhynchites*, also known as the elephant mosquito or mosquito eater, consume larvae of other mosquitoes as well as other aquatic organisms [ADDIN EN.CITE <EndNote><Cite><Author>Amalraj</Author><Year>2005</Year><RecNum>169</RecNum><Display Text>(Amalraj et al. 2005)</DisplayText><record><rec-number>169</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1508505122">169</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Amalraj, D. D.</author><author>Sivagnaname, N.</author><author>Das, P. K.</author></authors></contributors><titles><title>Effect of food on immature development, consumption rate, and relative growth rate of *Toxorhynchites splendens* (Diptera : Culicidae), a predator of container breeding mosquitoes</title><secondary-title>Memorias Do Instituto Oswaldo Cruz</secondary-title></titles><periodical><full-title>Memorias Do Instituto Oswaldo Cruz</full-title></periodical><pages>893-902</pages><volume>100</volume><number>8</number><dates><year>2005</year><pub-dates><date>Dec</date></pub-dates></dates><isbn>0074-0276</isbn><accession-num>WOS:000235006100012</accession-num><urls><related-urls><url><Go to ISI>://WOS:000235006100012</url></related-urls></urls></record></Cite></EndNote>]. In addition to arthropods, nematodes can also prey upon mosquito larvae. The nematodes from the family

Mermithidae are generalist parasitoids infecting a number of mosquito species [ADDIN EN.CITE ADDIN EN.CITE.DATA]. Because *Ae. aegypti* usually uses man-made containers such as gutters, water containers, cans, and tires as breeding sites, there appears to be no specific predator that preys upon this species but rather predators that are generally opportunistic and feed on larvae if and when they encounter them. Therefore, it is unlikely that a reduction in *Ae. aegypti* would adversely impact nontarget organisms. To evaluate the direct impact on nontarget organisms through oral consumption of OX5034, a submitted study directly tested the potential toxicity of OX5034 mosquitoes to an aquatic invertebrate. A feeding study examined the American signal crayfish (MRID 50698707) and found no apparent or measurable toxicity to the test organisms when fed OX5034 mosquitoes over a 96-hour test period. Given the limited timeframe and acreage associated with the experimental permit, and the lack of identifiable toxicity mechanisms, EPA believes the direct risk from OX5034 mosquitoes to aquatic invertebrates to be low. However, as many of the aquatic insects that may consume OX5034 larvae are larvae themselves and thus more susceptible to even low-level toxins, additional certainty regarding the lack of toxicity to aquatic insect larvae could be gained through a larval feeding study prior to a Section 3 registration.

In terms of vertebrates, while it is not known that any have evolved to specifically target *Ae. aegypti* mosquitoes as a major portion of their diet, in some instances, mosquitoes can constitute a significant source of prey. For example, amphibians have the capacity to consume large quantities of mosquito larvae, and a study showed that in the laboratory, 200-400 3rd instar larvae of *Culex* species per day could be consumed by salamander species. However, these numbers were seen when the *Culex* mosquitoes were the only food source and there was no prey choice [ADDIN EN.CITE

<EndNote><Cite><Author>DuRant</Author><Year>2008</Year><RecNum>151</RecNum><DisplayText>(DuRant and Hopkins 2008)</DisplayText><record><rec-number>151</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1508439619">151</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>DuRant, S. E.</author><author>Hopkins, W. A.</author></authors></contributors><titles><title>Amphibian predation on larval mosquitoes</title><secondary-title>Canadian Journal of Zoology</secondary-title></titles><periodical><full-title>Canadian Journal of Zoology</full-title></periodical><pages>1159-1164</pages><volume>86</volume><number>10</number><dates><year>2008</year><pub-dates><date>Oct</date></pub-dates></dates><isbn>0008-4301</isbn><accession-num>WOS:000260166800009</accession-num><urls><related-urls><url><Go to ISI>://WOS:000260166800009</url></related-urls></urls><electronic-resource-num>10.1139/z08-097</electronic-resource-num></record></Cite></EndNote>]. In the field, the Tiger Salamander, *Ambystoma tigrinum*, was found to readily consume mosquito (*Culicidae*, species not identified) larvae based on 26% of analyzed stomach samples containing remnants of larvae [ADDIN EN.CITE

<EndNote><Cite><Author>Brodman</Author><Year>2006</Year><RecNum>498</RecNum><DisplayText>(Brodman and Dorton 2006)</DisplayText><record><rec-number>498</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1583423343">498</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Brodman, R.</author><author>Dorton, R.</author></authors></contributors><titles><title>The effectiveness of pond-breeding salamanders as agents of larval mosquito control</title><secondary-title>Journal of Freshwater Ecology</secondary-title></titles><periodical><full-title>Journal of Freshwater Ecology</full-title></periodical><pages>467-474</pages><volume>21</volume><number>3</number><dates><year>2006</year><pub-dates><date>Sep</date></pub-dates></dates><isbn>0270-5060</isbn><accession-num>WOS:000239609400014</accession-num><urls><related-urls><url><Go to ISI>://WOS:000239609400014</url></related-urls></urls><electronic-resource-num>10.1080/02705060.2006.9665024</electronic-resource-num></record></Cite></EndNote>].

However, it is important to note that *Ae. aegypti* is but one of hundreds of species of mosquitoes and it does not appear that the salamanders noted above feed significantly on *Ae. aegypti* larvae. Mosquito larvae are also eaten by a number of fish including guppies, bass, catfish, bluegills and even goldfish. The most effective species for eating mosquito larvae are the mosquito fish, *Gambusia affinis* and *Gambusia holbrooki*, which are specialized predators. Due to the preferred larval habitat of *Ae. aegypti* mosquitoes, exposure to vertebrate predators is expected to be limited therefore also limiting the role *Ae. aegypti* play in the predator diet. A submitted study directly tested the potential toxicity of OX5034 mosquitoes to guppies (MRID 50889408) and found no apparent or measurable toxicity over the 14-day test period.

Due to lack of plausible toxicity and the generalist nature of most predators that may feed on *Ae. aegypti*, direct and indirect adverse effects are not expected in aquatic nontarget organisms as a result of release of OX5034 male mosquitoes.

c. Microbes

EPA also considered the possibility of the spread of antibiotic resistant bacteria in the environment from the release of OX5034 mosquitoes. The OX5034-tTAV expression is made female-specific by inclusion of a splicing module that has been linked to the tetracycline-off (tet-off) system. The tet-off system activates tTAV expression in females in the absence of a tetracycline analogue resulting in a lethal phenotype, therefore all OX5034 females die in the absence of tetracycline analogues. However, if a suitable tetracycline analogue is added to the larval rearing medium in sufficient quantities, tTAV expression is repressed, allowing for normal development of females to adulthood.

As the OX5034 colony in the UK will be reared using antibiotics, the presence of antibiotic resistant bacteria in the mosquito microbiome of the OX5034 colony is possible. Therefore, a consideration is whether vertical transmission of antibiotic resistant bacteria could occur and OX5034 male mosquitoes for release could acquire antibiotic resistant bacteria through this route. While OX5034 eggs shipped to the United States could have some bacteria on their surface, any bacteria that survived shipping would likely comprise only a negligible portion of the OX5034 microbiome. This is largely due to the fact that, although some organisms directly acquire their gut microbiota from their parents, mosquitoes predominantly acquire their gut microbiota from their environment as larvae [ADDIN EN.CITE <EndNote><Cite><Author>Strand</Author><Year>2018</Year><RecNum>496</RecNum><DisplayText>(Strand 2018)</DisplayText><record><rec-number>496</rec-number><foreign-keys><key app="EN" db-id="9d4fe52dcp9s9xe99drvp0fnwz0sz59xdwa5" timestamp="1583271537">496</key></foreign-keys><ref-type name="Journal Article">17</ref-type><contributors><authors><author>Strand, M.

R.</author></authors></contributors><titles><title>Composition and functional roles of the gut microbiota in mosquitoes</title><secondary-title>Current Opinion in Insect Science</secondary-title></titles><periodical><full-title>Current Opinion in Insect Science</full-title></periodical><pages>59-65</pages><volume>28</volume><dates><year>2018</year><pub-dates><date>Aug</date></pub-dates></dates><isbn>2214-5745</isbn><accession-num>WOS:000452865800011</accession-num><urls><related-urls><url><Go to ISI>://WOS:000452865800011</url></related-urls></urls><electronic-resource-num>10.1016/j.cois.2018.05.008</electronic-resource-num></record></Cite></EndNote>] and the environmental conditions for the development OX5034 males for release does not contain antibiotics.

Although tetracycline analogues will be used in OX5034 colony in the UK, no tetracyclines will be used in facilities used to produce OX5034 male adults for release at the proposed EUP sites (MRID 50698715). Additionally, no tetracyclines will be used in the release devices for field deployment of OX5034 mosquito eggs. A lack of tetracycline in release devices for field deployment is done

intentionally as this ensures male-only OX5034 mosquitoes emerge for release (MRID 50698701). The lack of antibiotics used in the facilities or release devices for OX5034 males means that there is a lack of selective pressure for antibiotic resistant bacteria to evolve. It also means there is a lack of selective pressure to maintain any antibiotic resistant bacteria that may have been on the eggs shipped from the OX5034 colony. Consequently, it is unlikely that OX5034 male mosquitoes for release would contain antibiotic resistant bacteria in their microbiome as no antibiotics are used in their direct production.

Therefore, due to the lack of antibiotics used in release devices or in the production of OX5034 male mosquitoes for release, coupled with the fact that mosquitoes generally acquire their microbiome from their environment, the risk that released OX5034 male mosquitoes would spread antibiotic resistant bacteria in the environment is very low.

3. Impacts on endangered species

EPA has determined that no adverse effects are anticipated for nontarget organisms as a result of the experimental permit to release OX5034 mosquitoes. Therefore, since adverse effects are not anticipated to nontarget organisms, a "No Effect" determination is also made for direct and indirect effects to federally listed endangered and threatened species, and for their designated critical habitats.

III. HUMAN HEALTH & ENVIRONMENTAL RISK CONCLUSIONS

EPA has reviewed the OX5034 manufacturing process detailing, amongst other things, the production and quality assurance processes used in the development and manufacture of OX5034 mosquitoes, associated standard operating procedures, and other pertinent information characterizing OX5034 mosquitoes on a genetic and phenotypic level. EPA determined this information to be adequate to support an EUP.

The human health assessment considered data provided on the mammalian toxicity and allergenicity of the tTAV-OX5034 (active ingredient) and DsRed2-OX5034 (inert ingredient) proteins and the potential routes through which humans may be exposed to these substances as a result of OX5034 application. While no determination has been made on the potential of either protein to pose mammalian hazard, the human health risk was found to be negligible, as exposure to female mosquitoes carrying these traits was determined to be negligible. This assessment was based on the demonstrated 100 % penetrance of the lethal trait in OX5034 homo- and hemizygous female individuals of the LWT background as well as in hemizygous individuals collected from the field, combined with the analysis of potential oxytetracycline sources in the EUP locations and the subsequent recommendation of spatial separation of OX5034 release sites from commercial citrus growing areas and wastewater treatment sites. The geographic restrictions for OX5034 releases are practicable within the scope of this EUP, as ground-truthing of the specific release locations was performed, but not for a full registration under section 3 of FIFRA.

EPA has determined that no adverse effects are anticipated for humans or the environment due to introgression of OX5034 background strain genetics into the local *Ae. aegypti* population. EPA evaluated OX5034 mosquitoes for key traits that could increase the ability of mosquitoes to transmit disease, result in larger population numbers, or result in more robust mosquitoes. Based on a combination of laboratory data, meta-analyses, and a review of the scientific literature, EPA believes it is unlikely that the local mosquito population would pose any increased risk to humans or the environment as a result of releases of OX5034 mosquitoes and introgression of OX5034 background strain genetics.

EPA has also determined that no adverse effects are anticipated for non-target organisms as a result of the experimental permit to release *Ae. aegypti* OX5034 male mosquitoes. No direct adverse effects due to

consumption of OX5034 males by non-target organisms is expected due to a lack of identifiable toxicity mechanisms. There are also no indirect adverse effects anticipated from reduction in *Ae. aegypti* as a food source should the release of OX5034 mosquitoes successfully reduce the local *Ae. aegypti* population. In the case of *Ae. aegypti*, their status as invasive species and their oviposition choice behavior makes it less likely that they serve an integral role in newly invaded ecosystems. Additionally, *Ae. aegypti* are regularly subjected to other control methods such as insecticide treatment and source reduction and it is therefore unlikely any predator species or plant is dependent on *Ae. aegypti* presence.

IV. REFERENCES

[ADDIN EN.REFLIST]